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(54) Title: BIALLELIC MARKERS (57) Abstract <p>The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.</p>		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO90/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given

- 5 polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e., the
 15 probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- These calculations can be extended for any number of
 20 polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

- 25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- The cumulative probability of identity ($cum p(ID)$) for each of multiple unlinked loci is determined by multiplying
 30 the probabilities provided by each locus.

$$cum p(ID) = p(ID_1)p(ID_2)p(ID_3) \dots p(ID_n)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- The probability of parentage exclusion (representing
- 30 the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and some of which exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ -squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),
20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod
30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154, (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different reference sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACACATGCCAGTTGGGAAGGCTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTTGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTC/TJAGTTTAAATGCTGTCTCTGTCAG
WI-7070	226	C	T	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATTCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-10744	61	G	C	GGGCAATTACCAGCAAAAGTCAAAATACCAGCATCAAGTCAGGTGCAAAAGGAGGTAGAACAA TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCAATGCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATAGTTCCTTTTCTCCCTCTTCTCATCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAATGTGTATGTATCAATTTGATCTTACTGAA
WI-9975	126	C	T	GCTAGGTTTGTCTGTGGCTGCTTCACTAGACTTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACATAGCTAGACCTTCCCTTCTCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCCCTTCTCTCCAGTTCATCCTGTATTAATTTCTCCCATATTAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAGAAATAAAGAGATCCCAAGTGGTGGG[G/T]CTT
WI-8010	247	G	T	GCCGGCCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTCCATCCTAGGATCTGCCTTAAAT CTTTGCTCTGTCTGA[G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222b	85	G	C	GCCGGCCTATCTTTTAAATTTAACTTGTATCTTTGGTGTCTCCATCCTA[G/C]GATTCTGCCTTAT AATCTTTGCTCCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGTCTCTTTGAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222	52	G	C	TATGCACCTCCACAAAGCGATATAATTTAAAGTTTTTTTTCATTAGAAATAATGTATAAAAAATAA ATATGTTATTATAGGCATTTATTACTAATATAGTCTCTTGGAAAGGACACCCCAACCAATACTT ATAAAGTACATGTAAATTTATAGTAACATAATTTACTATACATATGGAATAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-8007	242	C	A	TCAGTTGCAAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTTGTAG TCTATATTCACACATATGAGTGAAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATTGA ACTGCTCACCACATATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTTAC ATGCTTTCCAAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC
WI-9823	97	C	T	

WI-9651b	105 A T ...				TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTCGGAATTCCTTCCT ACTTGCTCATGTACAAATTTCTGCTGCTCTTCA/TJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTG TCTTAAACCTGTATGGTATATTAATCCCTGGTGTGAATGCTCTC
WI-9651	139 T C ...				TCTACATTCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTCGGAATTCCTTCCT ACTTGCTCATGTACAAATTTCTGCTGCTCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTGT CTTAAACCTGTATGGTATATTAATCCCTGGTGTGAATGCTCTC
WI-7676b	309 A C ...				GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTCTGCTGGGACCTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTTCTGTGGTGGTGGTGGTGGTGGGAGGAGCGGTGTGGACTGCAGCTTCTGCTGTGCTG TCCCTCCCTCCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ...				GTGACCTTCCTGCAGCGTGAGATGGCACATCCTTCTGCTGGGACCTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCGTGGCTTCTGTGGTGGTGGTGGTGGGAGGAGCGGTGTGGACTGCAGCTTCTGCTGTGCTG GTGCTCCCCCTCCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ...				CATTATCTGTCTTGGTCTGTTCAATTCATCTTCTCTCTCCTCAATGAAGAGGATAATTAAGCATCAT CATCTGGCCCTTTTGTGATTTGAATATTTTGTG/TJGACTCCTATGCACATGATAAATTTGTTA TGCTGTCTCTATCTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTTT
WI-9986	42 T C ...				TTGGTGTGAACCTCAGAAATAGGGAAAAAAGACAAATTTGA/TJ/CJGTACCCAGGAAACAAAGAG CCCTGCACCTGACTCCAAAGGAGTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ...				GTCTATTGAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTTCCAGAGAGCTGAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTTGCATGGCTCTATCCCTCTGCTCTC/CJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134 T C ...				ATAACCCCTTGTGTATGATACCCCAACTCACTAATTAATCACTTATGTCTATCAGATATCCTCTCT ACCCTCAGTTATTTGAAGAAAAATCCTAAACATCAATCTTCCATCCATAAAATGTCAGCATTT /CJATTAATAAACAAATAACITTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	---	TCCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTATAACCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTAATAAGCAAAGACCTGCA/A/C JCCTGGCTTCTGACTCCAAAGCTTATCCCTCTCATGCTGTGCTCAGCCAGGACCCCATGCCGA GAAAGCCCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCAATCAGTGAAAACCTGTGGGTATAGAAATGGAATGGAGATTTCAAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGCTCTAGGCATTGAAACCATCACCTGGTTTGCATCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T --	---	---	AAACACACAGAATCATCAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCAOCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTCACCTCTCAGCAAT TGGTCTGTTTCACTTCTATGGAACCTCTCCGTACTGTAAATTTTCACTTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACCTTTGATCAGTGGAAATAGAACACTTTGAATGGTCTTGTCO TTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAAGTAGCAATGGGAATGAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAACCAAGAGAAAAGAACTTGAT
WI-4719b	107 T G ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGT[G/G]ACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAG TGCTCAAAATTCCTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	---	TCAACAGCCTTTATTGOCACCTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCTCTGCACACTGCCAAGT TAAAGAAAACCTGCTTGTGCTGGAGAGGGAGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACCTTCT[G/C]ACTGCAGAGTATAGGACACAGGGTTCCAACTTT
WI-9484	178 G A ---	---	---	TCAACAGCCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTCTGCACACTGCCAAGT TAAAGAAAACCTGCTTGTGCTGGAGAGGGAGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCACCTTCTGACTGCAGAGTATAGGACACAGGGTTCCAACTTT

WI-7330	207 C T ---	---	---	AGGATGAAGGAGACACGGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAAATGTGGCATATAGGTTT GTGACACAAGAAAGTCATCTTTGGTGGCTAAGTTTACTAAGGAAAAATACTGAAAGATTAAAG TGAGAG[C/T]TGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
WI-9443	211 G A ---	---	---	TTAAAACAGTTTCAGGTTGTGAAGCAGAAAGGATGTGATTACAAATTTAAATGAATCAGTCACATT GCACAAATTAATCCTCTTGGCATCATACAACTGGGTTTAAATGGCAAATGATGACATCATAGCATGA CCAACTCATGGAAGGAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAAGGCACTGCAACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCATGCCCACTT
WI-7166	59 C T ---	---	---	TCCTCAAAAGAGAAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTTCCCTGTGCAAAATATTTGACTATCTGTATCTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAACTTGTGCTGTGAACAAATGTCGAAAGAGTCTTCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAGGCCCGAG
WI-7259b	189 T C ---	---	---	GCTCTTCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGAGGCTGCTCTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAGT[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188 G T ---	---	---	GCTCTTCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGAGGCTGCTCTCTCTCTGAGTTCTCTGGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTTAACCTGGCCACAG[C/C,T]TGGGGGAGCA GAGCAGCAGGTGGACAGGTGTTGAGGGGCCCAACTTCCCTGGAGC
WI-7322	275 A G ---	---	---	GTACTTTAGGCTGTGAGGGTGGGCATTTAGTGTGACCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAACTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAACTGCCTAAGCACTCAGGCCTCCCACTCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGATTTGTATGGGCTCTGGCTG
WI-7685	46 T C ---	---	---	TCAGTTCTAGTCTCTGGGGCCACACAGAACTCTTTTGGGCT[C/T]TCTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCTCTACCTCTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTGAGCTGTTGCTCAGTCCGCCAACAGATGCTTTTCTGTCTC
WI-563	87 G A ---	---	---	TGTGACCAATTTATTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCCTCCCT[G/A]CCCTGATCATGTCTACCTAACTGCCTACTTAACAATACTACTCC TGTGGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCCACT GCCCTCAGTAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCAGAT

WI-931c	191	C A	---			GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTCCAGTCTTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCC[C/A]JGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81	A G	---			GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTCCAGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-931	31	A G	---			GACCAGGGCACCAGAAAGCCACGGAGCCAC[A/G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTCCAGTCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTACTGTTGTATGGATTATAATTATGTCCAAAAAGCCCGAGCCTGG TACAGAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91	C T	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCACTTAAATACGTTGCCCCCC
WI-10870	103	G A	---			GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAG[A/G]ACGTGGAGTACCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAAATAAGGACATGGGTGAGC CTGAGCCACTCTTAAACCATGAACCATCACCACTTAAATACGTTGCCCCCC
WI-7719b	281	T C	---			AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCAATGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTTGCCCATGTATAATCCTCACTGATTTCAAGCTAAAGCAA
WI-7719	163	A G	---			AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCAATGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTTGCCCATGTATAATCCTCACTGATTTCAAGCTAAA
WI-10396	72	C A	---			GCCTTGGAGTATATCTAACTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTTCTTTTGTTA TGCCATTTGAGGGATTGATTTCTTAAACTATGAAGTACTGGCTGTCTCTCTCCATTGCTGTTGAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G	TCCCTTTATGCACCCCAAGAGATATTTATTAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCCCGTGGCACTCATGGAGGGGCGJTGCAAGTTGGAACATATGCAGTGTGCTCGCGGCAACACA TCCTGTGGGCCCCCTACCTGCCCCCAATTCAATCCTGCCAATAATCCTGTCTATTGTTTCATCCTG GAGAAITGAAGGGGAGGTCAAGTTGTTTGCAATGATTTGTCAGAGAACCT
WI-7842	57 T C	CACAGCCATGCCCTTGAGGAGCCGCCACCAGATGCTGAATCCCTATCCCATCTCTGTCGATGAG TCCCAITTCCTTGCAATTAGCAATCTGTCTCCCCCAAAAGAAATGTGCTATGAAGCTTTCTTCTCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTTCAGCTCCCTTATA
WI-7721	145 A C	CTGCCATCATCAGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGCGAGTGCAGCCCTTCTCTCC TGTCTCTGC/ACJCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGTCTCTCTCATCCATCTCTTACTGGGGCTGGGGCTAGCCAA
WI-4767b	173 C A	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCTCT CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGGATGACA/C/AJAAATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA/AGJATTCATAAGAGTT CCTCAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGAGTGGAGTGGAGAGGGTATG TTTCTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA/CJTGATGCAAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C	ATTGCACTGAAGTTTTTGAATACCTTTGTGTA/GJATTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A	ATTGCACTGAAGTTTTTGAATACCTTTGTGTA/GJATTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---	---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248 A G ---	---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATT[G/A]T
WI-7718a	42 A T ---	---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGC[A/C, T]GTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCGAGGAAGGAAAACTATGTATTAA
WI-7227d	99 G C ---	---	AGGGAATTGTGTTGCTCCTCGAGGAAGCCCGAGGCATCAATAACAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTT[G/C]JAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---	---	AGGGAATTGTGTTGCTCCTCGAGGAAGCCCGAGGCATCAATAACAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---	---	AGGGAATTGTGTTGCTCCTCGAGGAAGCCCGAGGCATCAATAACAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTCACTTTTCAGACAAG[C/G]JCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---	---	AGGGAATTGTGTTGCTCCTCGAGGAAGCCCGAGGCATCAATAACAGCCAGTAGGTCACCTGGC TCCGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---	---	CCCAATGCCTCCTCCACGATGTCAGGACTCCTGTCTGCTGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTATGATCCTTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGTGGGAGACAAAGGAACCTT/A JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACCTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCTGTGGTTGATAATAATCA GATATGCCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATCGGTCC CTGAGGAGAAAATCTGGAGGAGCTGAGGTGATGAAGGTGTATTTGGGAGGGAGCACAGTGT CTGTGGGAGCCAGGAAGCTCTACCAAGATTGGTGAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCTGTGGTTGATAATAA TCAGATCATGCCAAGACGGCCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAAATCTGGAGGAGCTGATGTGATGAAGGTGTATTTGGGAGGGAGCACAGTG TCTGTGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCTCTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCTC/GTCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACAGGCCTTGAGCAGAAATTTCTGAGACTGAAGGGAAATCCCTC/GTCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGCCAAGGAAGGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTTCGGACCTCATATTAAATAAGAGCAATGAGAGCGGAGGAAAATTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTTCGGACCTCATATTAAATAAGAGCAATGAGAGCGGAGGAAAATTGAACCTCTCTC AGGTACTGACTGTGGACCCAGACAAAG/GA/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTCCCATTTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC

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WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGTTCTTCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTCTGCTTTGCAGAAAGAAAGTC/CJC GTCTACCATTTTCAACAAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCCCTTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGCTGGTT/CJCTTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTCTGCTTTGCAGAAAGAAAGTC GTCTACCATTTTCAACAAAATTCGTAGTACAAATTTAAGTATCTCTGTTATCTCCCTTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 GA ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCATACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACAGGCCCGGACATCTTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136 GA ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCATACATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACAGGCCCGGACATCTTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141 C T ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCATACATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTACAGGCCCTCTTACAGGCCCGGACATCTTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116 GC ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCCTGGTCTCTCATACATTGCCA CCACGTAGCCCTCCCTTCCCTTCCCTTACAGGCCCTCTTACAGGCCCGGACATCTTCTGAGACTCCC ATGGATCATTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52 GA ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG/AJATACTAATAA AAACCCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATCACTAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATATTTAATTCAGTTTCTCAAAAGGAATATGAAATTTGTT AAATGCAATCCAGCTGTAACCTTTTTC/GGACTTGCTTTATTTCTT

WI-1126a	97 T C ---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATCACTAATAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATT/CJCAATATATATCCAGATTGTTTTCCCGCAAGAAAA ATTTATTTCTCAAGATATAAAAAATAAATAATTAATTTAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTCTT
WI-11183c	124 C T ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTC/TACTAACA TTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAAT/CJATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAATTTTGGAAAAAGTTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACA TTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGTGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTGCTTAGTCTTATTGTCTCAGTCTTGAGTTCTCCCTTTCTG/CCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTCAACCAACCTTCTTTTATTCTTCAGGACACTCAGTTACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-10770a	49 G T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTCAATCTCGCTTGATCATGG TTATCACTGGACA/CJTAGCCACCTCCCGAGCGCTTAGAACTCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAITCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGCTCATGACACTTTCAATCTCGCTTGATCATG G/CJTATCACTGGACACACCACTCCCGAGCGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAITCT

WI-10400d	189 A G ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCAGJTGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	188 A C ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCCTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---	---	ACATTTTATTAGCAAAACAAATCAGCAAAATAATAAATAGAAAGTAATTGCATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGTTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---	---	AAAGGGCTACAAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA/C/TTAGAAAAGGGCAATTCAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-10809a	33 C T ---	---	AAAGGGCTACAAACTAAGGCCAAACCAATGA/C/TGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAAGGGCAATTCAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGACACATGACATAGGCTTAA
WI-7038c	266 T C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATCTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAAGCTGTCAGGAAGGTCGGAGTCTGTAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATCTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAG/A/C/GACTGTCAGGAAGGTCGGAGTCTGTAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAACCAAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCAATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCCTTCACTTTGCAATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGACGAGCGTCTCTAGAA TCCTGACTGTTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGTGGCCAGGGTCGGGCTCCACACA[C/T]AG CCCTCAGCCCCCTTCACTTTGCAATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAATACAGATCCCAAGTCTCCTCTCTCTGGATTGGATCTAGCAAGACCAGACGAGCGTCTCTAGAA TCCTGACTGTTAAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATCTCT[G/A]TGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTG TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAGGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCATCTCTGTGGGATAAGGTGCCATTTGTTCTTGGAGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTGAATAGTATGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTGAAT TTCATATACCTCCATTATAATTCATATCATCTGACAGAGAAAGACACGGTGCCAACTGGGTT TGTTGGTGGCTGCACACCCACA[G/T]TGGCAACTAAGTGTAACTCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAATGCTTGGTTATTTGACTCCAAAATTC/TGAATAAGTATGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCACTCT GAATTCATATACCTCCATTATAATTCATATCATCTGACAGAGAAAGACACGGTGCCCAACTG GGTTGGTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTAACTCTCTAAA

WI-10613b	172 A C	ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTGATTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTG[A/C]GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTGGGACTTAGGATGTAG
WI-10613a	44 G A	ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]GTGAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTGGGACTTAGGATGTAG
WI-7587c	133 A T	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA[A/V] TJGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGAAGC ACATCCCTTCTG[A/J]ATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T	GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTCTTTCCAAAGTGACTACCCCTTGA AGCAGATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAAGAAATATCCAAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTGACTACGCAAACTCAATCAGCCAAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC[T/A]AAAGACAGCCATTTTAACTCAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-10681a	41 A T	ATGACTCAGGTGACAAAAGAGCATGTCTAGACCCCATTG[A/J]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTCAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAAGAACTTCAAGGTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTGGAGAAGGAGGAGTGACGCTCTGTAAAAG
WI-7222c	126 G T	GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGCTGCTTGAATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTCTCAAGTTGGGGATGGG[G/T]AATAA AGGAGGGGAATTCCTTGAACAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255	G A	---			GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCOCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAATTCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTCTCA
WI-7222a	126	G T	---			GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCOCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTT
WI-8054d	41	C A	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTC/AJTATCTCCTCCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTTCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGTTTTCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTTCCTGGCGTACAGA[G/TAATCCTTGGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAGCACAA TCTCTTTGTAGT[C/TTTAGCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGCGTACAGAGAACTCCTTGGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTAGAACTGGATGACCTTGGCCCTTCTCTTCTATCTCCTCCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCACTCTTAGATCTGCAGTTGGCTCAACGCACCTCAAGCCTTAG[C/GJA CAATCTCTTTGTAGTTTTCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTTCCTGGCGTACAGAGAACTCCTTGGCCCTT
WI-10854b	152	G T	---			TTCCACAAAACCTCCCTGGGCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAGACGATAGTTAACGCTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/JGGAGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T	---			TTCCACAAAACCTCCCTGGGCCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACA[C/TTGAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A AATTTATATGAAGGGTTAGCAAACATATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTTGTG TGCCTGATGGCTTTGGTGTTCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATGAJGCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTTGCTGATTTCTAGATATTTAAA GGCAGAGAAGATCAGAAAGTTGAA
WI-9826	125	A T AATTTATATGTGAAGGGTTAGCAAACATATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTTGTG TGCCTGATGGCTTTGGTGTTCACGCAGTTGAGCCATTGTGACAGAGGCTGTTATJTGGOCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGAAAGTTTGCTGATTTCTAGATATTTAAAG GCAGAGAAGATCAGAAAGTTTGAA
WI-15986	60	T G	TTGTTTGTGT	TGACATTATAT	CGGACACGTGATATACAAATACAGATCGTATGGGTTTGTGTGTGGGTTTTTTTTTTT/GJTTAC ATTTCTTTTACGTTTATATAATGTCAGCAITTCAA
WI-8655	29	A G AG	AACTGCAAAT AGGAAACCAG	CCACCTGGGSC TCCC	TTCAAGTAACTGCAAATAGGAAACCAGAGJAGGGAGCCCCAGGTGGGACAAATCATGGCTACCCCG TCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCCTTTAT
WI-8170b	259	G A GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGAATCCTATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAC
WI-8172	136	C G GACA	CCTTTATTAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTTAAATTTGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAATTTCTGT	TGTTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTACATGAAATAAAACAATTTCTGTTGCJG/AJGCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGCCCGAAAT ATTAGCGTTAAAGGAG/CJTTGAGTTGAGTCAAAACACGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAGJG/AJGAGATGGTCAGGCTTCTCTG TTCCTTAACCAGCAGAGCCCAAGCAACCTAGAACGCCCTCACCTAGCCTCTTAAT

WI-8827	22	C T	TCCCTGGGAG ACTATGG	GGGATTAGGAT TTTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C]/JAGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCTTCTATCCACCAGTCTCT
WI-8833	51	A T	TCCTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCTCTTAAAGCTCTCTGTAGACTGTCTCTCCATGCGCATCTCTG[A]/JTGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCCTGTGCATAAAGGTCAGCTATGT
WI-8377	63	A G	---	---	ATTTTTAGCCATGTTGGTAAAGTTCATTTTCAGTACATGGGTAAACCCAGGCCCTTTCCC[A]/JT TATATCCAGGTATGCTACAAGTTCTTTAACTCTTATCAGAAGTTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAAATTCATTAGTTGGTTGTCTAATGCTCATTTATTTATCTGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCT	CAACAGGCA GGCAGG	GAGGGACTTAACCTTTGGCCT[A]/GCTGCTGGCTGTTGGCTCTGCGCTGCTGTTTGGTTCTT TCTCTTCTACTGGTCTTCTTTGCTTTTGCAGCCACCTATGCTGCTGT
WI-8853	79	C T	CCCGGGCATTG AGGATA	AGTCTTCTGA GCCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCATCTTCTAGCTTCTGGTTGATAACGCTGGTTAATCCCGGGG CATTGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52	A G	---	---	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGTCGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGTGACTGGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/CJGGTGAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8895	32	A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A]/CJCTCCGCTCTTTGAAATTTCCATTAAAGCA CAATGGGGTAAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93	G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATTTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/CJTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGGGACAGCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCTGCTCAGTCACCCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAAT[G]/JTTGTATCAGTGCATATTCTGAAA ATTATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATATATAGAAATAATACGCAGCTGTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAAT[G]/JTTGTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A]/GTCCCTCTGCTGCCCTGTCAACCCACATCCACAGAGCA GCCCTAGTCCAGGTGCGCCACTGCCACCCACGGACACGGGAACAGGCCCATGCTGC

WI-12108	40 C T A T A	TGAAAAGGG TAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCAATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTAA
WI-5989	29 G A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAAGGTACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTTAAAGAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCTCCATCTTTTCTTGGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGGTGGGGGTGTGACGCTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTTATCTGTACGGCAGCCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCTCTCTCCCCACATACCA ACTCTTCACCATGATGATTATACCAATAATACAGTTCCCTTATATGAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCTCGCTG CCTC	AGGGATCAA GAGAAAAGGC	TTTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT GTT	TCCTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTCAAGTTTCTAACCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[G/C]CACACTACCAAAAGAGAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAATTATTCTGATACAACTGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTCTGCTCATAATT[C/C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAAAT CA	AGGTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTCAC[G/A]CTTCCAGAATACAAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTCAAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGGAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTCGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATCCCCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGTAAGGAGCCCCG
WI-11324	40 C G T G T G C C C C A	GGATAAATCA TGTCGCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTCTTGTCC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGTTCGCTAGTGTCTACGAGAGGTACAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTGCAATCACCTGTGAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTACAGTCGTGCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGGCGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGAGCTTTCATATTCTGTTTTTAAAAAGTC TCTTCAGTCJAGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A A G T T C	GGTTTGAATTT ACACGTAAC	TGCTTGTATC CAAGTTAAAT	TCATGTGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAAATGAATGTTTG AAATTACACGTAACTAAGTTCICATATAATTTTAACTTGGATACAAAGGCAATTTGTTATGCTAAT
WI-11392	55	T G A T A A A T A C	GGTTATGTGTT CTTGAACITTA	GTACATTCACG TGTTTTGTAAA	TTCTATCATTCCTTAAATGGGAGGTTATGTGTTCTTGAACCTTAAATAATACIT/GCITTTTTACA AAACACGTGAATGACTTTCTTGTGAGAAGGGGAACACTGAGTCTCGCTCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTCACCCA	AAAGAAATAGATGGCATTTGTTTCAGTTAAATTTTGTGTTTGAATGGTGTGTTTATGATGGGTGAATA TGAAATAGCTTACCTCATCCACTCTAAAGGTAGTTGGTATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCACCAAC TGAGAAGCCA	TGCCAGGGCT TATTTG	CTGTAGCTTTTCCCAACTAAACGTGAGTCCAGTATGCTGGCAGCACGCTGTGTTCTTGGTG TATCCCATTAAGTGAATCCCAACCAACGAGCICAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26	C T T T A T T T G C A	TGAGAAGCCA TTTATTTTGA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAGTC/TCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	TTTTCTTTGTGCTCTTTTTTTTAGTAGAAGCAG/GGGAAACAGTTGTCAATACTACCTTCTGTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAATGTCA
WI-11276	41	A G A G A G A C	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GCGGTG	AGGCAACACTGCTTTATTAGCGCGGCGAGCCAGGAGCAGACAG/GCACCCTGCTCCTCAGTACACATT OCCCCACCCCTGCTCGGTGCTCCCACTCAGGGCTGGCATGGAGGGGCGAGCTAGGCTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCATAG/GGGAAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	AATGGCTGTTTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAGACACATACGGGTACAAAAATTACA GGTGGTTAGTTCAATTACATGAGTACAAAATCAATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGAT GGAAGACAC	AACTAAACCA CCTGTAATTT GTAAC	AATGGTCTGGTTTTATTGAGAAGCTGTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAACCTTGAGCTTGCAGAGAACACATTTGTGGGCTT[A/ G]TTCAAACATGGACTGATAGTCCACCCCCAGATTTCTAACTGGTAGGCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCCT TTCTGACCAGCTGGCTTGGCACTTTGTGAGATTTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTAG TTCAATGAATA ATTCAA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAAATTTTTCAGAAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAAATTTATTCATTGAACATAAACAACCTTAGCAGAGGAAGGACCTTTTGAT
WI-12310	46	G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTGGGTCCT AAA	TTTGAAGAGATGCTGAATTTATTTCCCAAGTATAATTTTAAAGCT[G/A]TTTAGACCCCAACATA TTTAAACATCTCTTACACATACAGAATTTTCAAGTTTACAAATATTCAGAGGCAATTTTCTTAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATTT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGAAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAACCTTG GATTT[C/T]CCAAAGACCCGAAGACTCCTCCAAGTCTCACTGTTAGTAAGGTCAATTTGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTTCACAGGTTGTATTTTGTAAAGATTTGTCTATCTAAATTTTCATATTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[G]GGGATTTTGCAGACTTTCTCTC
WI-11585	79	T C	TGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATCTTCC	TTAGAAGGAAAGAAATAAACAACCGTAAATGGGAAATCAGTTCAAGGTAGGAAGGAGCTGGGTT TGCAAAACAAAAAT[C]GGAAGTATCAGTGAAGCATGGCCTAGAACTCCAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108	C A	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTCCCAACCTGGACTTGCCAACTTCACTGTGAAACTGCAAC[C/A]ATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGTGGGAAC ATGCC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCCAACCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83	T C	TTGATTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAATAAAAT[C]TACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAAATTGGCAATGA

WI-11626a	39 G A G	TCACCTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTTAAAAATAAATACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAATTTGGCAATGA
WI-11627	23 T C A T T G T C C T C	CCTTCCCTTC CATTGCAACC	CATCTCAAG CATCTCAAG	ACCCCTTTCCTCCCATGTCTCTC/T/CJCTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAGGG AGATGAGAAATAGTATGCTTTTGTCTGGCTTACTTCCATTCGATGTCAAGTCCATCCATG
WI-11636	61 A G T C C T	GGACTTAAAA AGATCTGCTTA	AGAACTTGGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAACTACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119 C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAAAATAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCATC/G/JATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37 G C C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGITT	AGTAGAACATCAGTGCCAAAAGACTATTACGAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTACAGAGTTCACACTCATATTTTCATATTTTT ATTTTGGGTGTGGGT
WI-11656	28 G A A A	ATTGATTTTAG AAGGAAGTGC	CAAGGCTTGT CCTCAAGTAA	ACCTGATTGATTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAAATGTCCTGAAACAATCAGATTCCAGCCTGGAT
WI-11680	55 T C ...		---	ACAGATACTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT/CJTTGCATAAA GGCTGGGAAGGTGTTTGGCCAGACCGTACATCTTTT
WI-11696	47 T C A G G G G A C A G	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACCTTGACATCTTTATCACAGCAGGGGACAGT/CJAGGTTGGCTTCTCTA ATGCCCACTCTTGTTTTCAGAACTTTCCACTTGGCC
WI-11702	69 C T C A G C A G	GAATAATACT GAAATAACCA	AGAACAACIT AAGCAAATTTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACCTTTCAATAATTAATAATCGAATAACTGAAATAACCCACAGC AG[C/T]TTTTCAGTATAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTCTGCAGA
WI-11706	60 C T T T C T T C T T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTCTCTTCTGTACAATTTATTGCTGCTGGCTG GAATTTGTTCTTTGGTGATTTGTCCCTTGTCTGCT
WI-11709	105 T A T T C A G T T T G C	AGAAAGCTTGC ATTCAGTTTGC	TCATTTCTTCT AATTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAAATGAGAGATTATGTCTTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGTCT/AJGTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103 C A C A G T C T T C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCAAGCTTTCCAGCACAAACAGCCAGCCACACTCTAGACACGCTTCAG TCCAGTCCATTTCTGGCACCTAGCCTCAGTCTTCACTC/AJCTCCTCCTCCTCCACACACTCCTTC

WI-11715b	123	C T	AGCTGGCTGC AGCTT	TOCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGGAAGA
WI-11715a	49	A C A A A	GCACACAATG TAAACAGAC	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAA[A/C]TGCAATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTTCAGCCAC AGGATGGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A	AACAATCCTT AAAACAATA	CCTGTGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAACCACAGGC AAATGAAAAACAGATGCCCCAGACAGCACCCACCACATGGCACAC
WI-11728	16	C G ...	ATCTGTGTTT TCGCTG	...	TTTTATTATCAAACT[C/G]CAATTCATTTCCAAATGTAAAGTTATCATCAGCTCCCATCCACTTT CTCCCATCTTCTATCTCTTCCACCCCTACACTTCTCTCCCTACAACCCGGTTCCAA
WI-11758	61	A G	ATCTGTGTTT TCGCTG	TGATTGGCCCT GTGGTCTA	TTTTCCCTCTTTTAAAGTCGCTATATACTAGAGGAGAATCTGTGGTTTCGCCTG[A/G]TAG ACCACAGGGCCAAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCCAAGATCACCATCA
WI-11295	37	A G A T A T A A	GCCTCACAAA GTATTTCTAA	AAAGTGCTCA TCTGTGAATC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT[A/G]TAGAGTTCCAGATGAGCACTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ...	GGCTCAGAGA GCAAGGGA	...	AGCATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACACGAGAGTCAGAGATTAAAGAAAT ATTATTGCCTCCTTTTTTCCCCCT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G	GGCTCAGAGA GCAAGGGA	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTTAATGGGCTCAGAGAGCAAGGAA[C/G]CACACAAAAATTTACAGTCTGA GTTTGCAGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G	CCCAACTTACC AAACCTCTG	OGGTAGGCGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T A A G T T T A A A	GTGAGGTATTT AGTTTAAATG GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAAATTTCCCAATTCCTCCCTTTTATAGTTTTTAAATGTGTTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATCTATTCTA[C/T]TTGACAGCACAGTCTTCCAAAGTTTGTATAGACAATCTGA AAATTGGGTTCTGAAC
WI-11906	52	A G A T C T G A A	TGTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTTATAACATCAAGAAAGAAATCTGAAT[A/G]TGAGGGAACGTG CAGAAATTAACCTTCAGTCTAATTTCTCAGAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78	A G	TTGTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGGTCAAGAG/GCTATTAGAAAAATCTCAGAGGAGGACAAATGATAGTGCACCTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60	T G	CATGAAGAGT GGGCAGTTCA	TCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATGCCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATGGCTTTACAGGAAGCATTTATGG
WI-11846	31	C A	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAAACTTCTTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAGGGAA
WI-11965	65	T G	TGAAGATCAG ATCTCTGGTTT ATTT	CAGCTGTGGTG AATGTTGAT	ACAAAAATCACAAGTACAACACTGCTTATTTTCTTGTCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90	T A A	TGCCCTACTAC GCTTTTAAAA TTTATT	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAAACAATCAGTTCTATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[T/A]AATAAAAACTGTAAACACATTTCTCATTCTCTTACGA ATACCTTCTTTTGATATTGCAAAATCTATGGCATACACAGAGGCACCTCTCAATGCCCTG
WI-11049	95	C T	TTCTGCTGAAGATCACAAAAACAATTTCAACCTCTGTGGTTCAAAAAATTTAAGGATCTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGG[C/T]AGACTTCAGAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCA[T/T]GTAGGAAGGAACATTTCAAAAGCCCA
WI-15488	69	C T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49	A G	AACAGTTAAT GAAACACATC OGT	GGCTGGTGAAA TGATGTAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[A/G]GTATGACATCATTT CACACAGCCAGCTACTTTCATGTGGCAGAAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135	C T	ATGAGACCCCTGCTTTGAACGTTTAAACGTTTGGAAATAATGGAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGGAA
WI-11070a	110	G T	CAGAAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTTAAACGTTTGGAAATAATGGAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTT[G/T]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAAGGGAA
WI-12020	121	T C	AATCTTTTATATTTCCAGCTTTGAGACAGTATTTTGAGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCAATTT[C/CT]CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGGAGCATGTGCATATCCAGAGGAGGAGAGAGAG AAGAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106 T C AGGCA	TOCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGGAGGAGCAT/GTGCATATCCAGAGGAGGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49 T C GGCATATTCA	GGTTATTCAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAAGGCATATTCAAT/CJTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAATAACA
WI-14267	28 T C	AATTATTGCTGAAATTAGGAAGGGAGCAT/CJTGAATGGGAAGGGGAGGTTAGAGAAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAGTATAAAACCTGTA
WI-13892	50 G A TAGAAC	TGATGATGTCA TATACTAAAA ATCAAAG	GATTTGTTTTATTCAATCTCGCTTTTCAATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATGATGAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108 C G TCCCTCTCTC	AAAAGCTTCTT TCCCTTGA	ACCTCTTTCTGATGACACTTGTAAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTTGC TACAAATTCAGGATGCGAGGCGATGAGAGGATTCCTCTCTC/GTCCAGGAAAGAGCTTTTGGC
WI-13951b	88 G C	AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCGATCAGAGGAAAGAG ATGGCTTTCTTGTAAATCTGGAGCAGATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39 C T CAAA	TTCTCTGATC TGGGGTCT	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAAATGAACATCCCTCAGCCCCCATGGCATGGTGATCCCTTCTCTTGGGATCTGTGAATATAOCCA ACTGTCTTGTCATGGC
WI-13264	25 G A TTGCCAT	GGAGGGAGAG ACGGGAATA	TTATTTGTCTATTAGCAAAAGGAGTTAAATACTGATAGA[G/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAAAGTAACTAAGTTGTTCACTGTCTTTCCCTCACAAGGAGTTGAGCCCTTAGATGAC
WI-13960	39 A C TGATAGA	CATGAAAGGA CAAATTTGCAT C	AACCTCTTTATTGTTAGCTAGCCCCAGTGACTTTTATGCATCTTATAACCAAGAAAGCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACAGGAACCCAGGCTTTGGCT
WI-15843	62 C T CAG	CTCTGGCTCAG ACTTGTCT	

WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCCACTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACACTCACTGACTTAACAGAAATGAACATCCAGGCACTCACTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACACAGCCAT[G/G]TACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTCAGGGTGAAGGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTGA ATGTATTCTCTG	TGAATAGTTGG CAAGGAAAA	AGATGTCAGTTGAATGTATTCTCTGAT[G/C]TTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGAAAAATATGAGTGAGACTCA
WI-14284	55 C T	ATTTCAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAACA[C/TT]ATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCAATTGA
WI-14288	85 G C CCCAGAT	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAATCTT	ATGACCAGACCAGAAGCCCTGTTCTATATGAAGACAAACAGGTGCCATACCTTGGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTGGTGGAGGAGACCATGACAGATGACAAACGG
WI-13522	33 C T ACAAC	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTGTAGTAGTTACCCCACTAATACAAC[C/TT]GAGAACCCTGACTTCAATATTATGAGAG AAATTAATCTCCAGGGAATTTTGCAGAGAGATAATA
WI-13529	42 T C TTACCA	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATCCACAACATTTATTGAACAGTTACCAIT/CJAAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTATAGTCTAACAGGGGAACAACTCTC A
WI-13859	84 G A	TTATTTGTCAGAAITTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTGAGGAAAGGACTCTCTAGAACTTGAGCA ACA
WI-13536	29 T C	TGAAAGGATACAGAAAAAATCAGCGAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCAACAGCTCCAGTTGCTCTCTCCAGTCCCATGAGTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAACATCTCAC[G/A]AAGTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCCAGAGCT
WI-13477b	61 A G	TTGGTTTTTAATACCTGTTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT
WI-13477a	32 A G AAGG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTGTTGGATAAAAGG[G/G]CATTGTTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTT	CTGACCTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG(A/T)AAATAGTTTCTGAAATGTGCACACTAGAATATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAAGAAATCAACA TGTGCACAAAAGAGTAAATTT(G)ACCAAAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGGA(C)ATGGAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGTGAAATCTGGGGCAGCTTCAAAATTTCTGCCTCTAAACATTTTAC CCAAATTTTCATTATTGCC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC(A/G)TACATTTTAGGTATCTGGCACAATTAACCAAAATGT CTGCCCATTTTGTAGCTTTTACAGTACAGATTCATTGATGTGCTGCCACATCTG
WI-15809	77 T G TGTAATGCC	TGGTTTCTGT TGTAATGCC	TAAGGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC(T/G)TTTACAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGTCGAAGAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAA(A/T)GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCCTTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATACT(G)GCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCCTTTATCCAAAGATGGGAAGC(G/A)CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATACTGCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAAGAACT GCTGAATGTCTCTCTC
WI-13763	59 T C GCAGTGAT	GGCTGGACACT	CCCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATT(C)AGGG GCAGGTGTGGGCGAGGTGGGGCTCTGAGCCGAGGACAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A ACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACC(T/A)AGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTCCCGAGGGCAAAAAGA GAGCTTCCAGAAACCTC
WI-13789	62 G A AGGGAG	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATTGGATGGCTGAGGGAG(G/A) GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGACAGATGGATGGTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAAGTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACAAAAAGC G/ATGCACAAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	GTTCTCCCACTACTCCGCGAGAAAAAGGCATATTCAA[C/T]TGCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCCACTGAA GACTCACCAG CCCT	GTCTCACTTTCTTGCTAGGCTGTAAATTTTTCAGTTTAAACAAGTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATCCCT
WI-13600	26 G T	TAATGAGCC AAGCATCCAT	CTCACITTAATGAGCCAGCATCCATG/TJCCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA ATATTAAT	GATAGGAAAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCG CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTAAATATTGTCATGAGGTATGCACCT GCCCCA
WI-13650	76 A T	AAAGATTCAC AATATTTCACT TTTAAAC	GCATTAAACATTTAAAAATTTCTGAGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTAC TTTTAAACIATTTAAAAAATACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAA	CAATACATTT GCATTTTCTA AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAGACATTTA/GITTCAGAGAAAACCTGGTATCATGCAGGAAAAGCAGAAAAAAT
WI-13909c	93 A T	ACTTAACTGGCTTATCTTCACGGTAATCTATTTCTGTATTTCCAGTGAAGTTTCTCTCACACT CTCTTCAAACTCGAATATCTTTT[C]ATGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTTCTGTATTTCCAGTGAAGTTTCTCTCACACT CTCTTCAAACCTG[C/A]AATATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	TTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAAATTAAG AATCAACATCATTTCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA GTTCCCAT	TTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTTATAAAGGGACAGAAAAAATTAAG AATCAACATCATTTCTGGACCATTGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA TCCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTCTGTTTGGAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

[illegible]

WI-13785b	40 C G	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27 T C TGCTT	AAACTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTAC T	TCAAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTTACCCCATTTGATACACATAAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	TTCTCACCCCT	AGAATGGGCTC TTAACCTTGA	TAGTCTCTACAAATCCTTCAATCCATTTCTCCTCACCCCTTTCTTTCTC[J/A/G]TACAAGGTTAAGA GCCCCATTTCTCAACAAACAAAAAACACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[J/G]GGCACTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAAGGTAAGTCCCTGTTTGAGCCCGGGGCTGCTCATTTGTTA
WI-13424	66 G A C	TGAGGTTTTTC ACCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCCTTGCACAAAGTCTCCCAACTGGTTTGGAGTTTTCCCTTCTGAGGTTTTTCAACCCTATTCTC[G/A] JTAGACCTGGGAGAAACAAACACATGTGTAAAGTGCTCAGGACATGAGGCGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGGCAATTT[C/G]AGATCCAGATTCAGCTTGCTCATATAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCTGAACATCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACTCATCA[G/C]CCTTCTGATTTTGATCCCTTTCTGCTCTGTAAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56 A C TGGGTGOC	TGAGCACATA	CCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[J/C]GCCCGAG ACAGCAGGATAAGTTTACAAAACCTTGACCAGGAGGTTAGAAGCAAGGCATGGTTCAAGGATG
WI-15702d	107 T C	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[C/J]GGGTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAAATGGGTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAAATGGGTCTTTGAACAAATAGTTT TGA

50

WI-15702a	48	48	AACAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAAATGTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAG[G/C]GGGTAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAATGGTCTTTGAACAAATAGTTT TGA
WI-13831b	113	113	T C ...	---	TTTTTTTTTATGGATGCACGTGTACATGTTTATTAGCGAAGGTGACTTGAAAGGAGATTACACAT ACTTCCACTGTATCCTCCGGTAAGTTTCTCTCTCTGTAGAT[C/G]GTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56	56	G C ...	---	TTTTTTTTTATGGATGCACGTGTACATGTTTATTAGCGAAGGTGACTTGGAAG[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGTAAGTTTCTCTCTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13806	62	62	G A ...	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAACTAGGCCCTCAGGT[G/A]C CCATTAAAGCATGCTGTGAATGCAAGGAAAGCTTAAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86	86	A G ...	---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTTATTCACATTATATTAATGCGATT TTTGTCAAATAAATAGGGA[A/G]TTCTCTTTAAATAACCATCTCTCACTTCATGGCCAGT
WI-14373	95	95	A G ...	---	AGGCTGTTTTTGAGGCTGAGGACCCCAACATGACAACGTAAAGACTGTAAACCATGTCATGTGAGTT ATGAGCTAGGAACCTCTGGACGAAACCA[A/G]CACATATACAAATCATCTCCACCTCCCAACGCTTT ACTTTCACAGCCTCTGCA
WI-14078	61	61	C T GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACACACATGGTGATCAAAGAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAGGACTTTAGATGGTCACG
WI-14083	47	47	C T ACAT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACT[C/T]ATTTGTTATTTTCACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTGGCTGAGTTGTTGCTTAAGGTCTTACAAGGCCAA
WI-14085	31	31	A G AGAAAA	CAGTCATGTT ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAAGAAAGAAAAAC[A/G]TAACTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAGTGAGTGAAACAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCTTT
WI-12169	121	121	G C TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAATTTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTTCTAAA TTTTCCACCTTTATGCTAAGTTATAAAATAAACTTCTATTTCTTTGCTT[G/C]TTTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50	50	A G ATC	AGCTGTAGTGG TCAAATACTCT AGAA	TTGTTTTTATTTGGGAGAAATGAAGGAGGAGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGTACTACGAGACCCCTGCTTATAGCCCCAACAGGAAATCCTCA TCTGCGGTTGOCAGACAG

WI-14379	102 C T	TCTATTAACA GGGTATGTCA CACC	ATCATCTGTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCCAATCCTAGTATGATTTCTTT TACITGTGCTATTAAACAGGGTTATGTCACACCIC/TGTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA/C/ACCCACCATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCGCCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22 C A	ACCGCAGAGCTGCTGTATTTAAA/A/GJACAAGCGTCTGCGAGGGCTGGGACCAGCTGC AGTGGGGCTCGGCACTGCTGCTCTCCAGGACTCTTCCACCAACCC
WI-15937	24 A G A	CGCAGAGCTG CTGTATTTAAA	GCAGAGATCCA GACGCTTGT	TGAAACTGAAACGTAATTTCTCCAA/CJACACCCGTAGAAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAAGGAAGTTTCAGGTGATACAAGATGTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24 A C A	AAACTGAAAC GTATTTCCCTCC	GGCCTTTAAGT TTCTACGGTG	ATGTTTATGATCAATTCCAAACATACAGTACAGGGAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC/A/GJTATTTTCAAAATGTGTTTCAAAATCTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92 A G	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTGGACGACTA/C/JGTGGCCATGCCATTCTGTAAAGTGAATTAATGAACA GTTTATTTCTCAGAGTTCTGGAGTTAGAAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGTCTTCTCACCATGTCTTCCATG/A/GCCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14138	23 C T	TGTTGGCACC TGTTGGCACC GCTTTCAGTAG TAGTATATTCA GACAATC	CAGTATGTACA GTGACATAACA TAGAACA GCTCATTCTT TTAGTGCTAAG TAATATT	TTGTTGTTGGCACCAGAAAGCTC/TATGTTCTATGTTATGCTACTGTACATCTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG GGCAGGTTTATTCATAATTTTCAAAACTTGGAAAGCAACCAAGATGTCTTCAGTAGTATATTCA GACAATC/G/AJAATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59 C T	TTTTTAAGAGTGCTTCCATCATTATTTATTTGATTTGCACACAAACTTTTTTAACCTC/TGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCC
WI-15953a	26 T G A T	TTTAAGAGTG TCCTTCACATC	TCATCTGTCT TGTTGTTTTG A	TTTTTAAGAGTGCTTCCATCATT/TGJTATATTGATTGACACACAAACTTTTTTAACCTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGTCTTTTGAGATAGAAGCCTTCTTCAGAAATCA CCTCC

WI-14631	82 G A ...				TGAATTCAATGGACAGTTTGGCTCTGTTTGTAGTGAACCCCTCACAGCACTCTGCATAGTCGGCTTTCTGTCTCTTTAAACG/AJTGCTGGTCCCTCTGCTGCCAACTTTAGGATTGGCCTCCTCAGGGCCTTGTCTGTA
WI-8053	24 A G ...				ATCACACCGTGTCTAAGAACAC/AJTGTTTCATGTCCAACTCATATCCCCGGGACTTTGTCAACTGCAGTACACTTCTGCACTTAACTGGCTTCTGTGAGGGAAGCTCCTAGAGCCAGGTAAGGGGGTGCAGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAAACCACGGAG
WI-15964	99 T A CTGGAGTA	GCTCTCTGTCC	GACTTCTCCAC	CCTCTTGC	CAGAAACCTCTTCTGTGTAATAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT/AJGCAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103 G A GGCAC	AGCAGCTGGG	CCCTTCTTTC	TCTTCTTC	CAGCTAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAAAATACCCATCAGAGCAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC/G/AJGAAGGAAGAGAAAGAGGGGGAGGAGCCT
WI-12179	96 G A TGGAGTCA	GGAGGTACGG	TGTAATGACCC	TGTAGATGC	TAATTTAAACACGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTAGAGGACATGAATAGTGATGTGGAGGTACGGTGGAGGTCA/G/AJGCACTCTACAGGTCATTCGAGGAGGAACAG
WI-14651	49 C G ATTGT	TCTCATTTAAA	CTTATTT		CACAAATAGTGAATATCTGAGCAAGAATCATTTCTCATTTAAATTTGT/C/GJAAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105 T A ...				AATGTGGACTTCAACAAGGGTTTAAACTAATCTAATACAACTTCTACAACACATTTCCAGAGCATATAACAAGAATATTTACAGGCAGCTAATGTATTTAAAT/AJAAACCATGAAGAAAGAAAACTTG
WI-13473	31 C T ...				ATCTAGATGTCAGCAATGGGCTGAGACTGT/CJTGCTGTGTAGATGCAGTGTGTGTATTTCTTCTACCTATTACAAAAATTAACAGAAATATGGCTTGGCTTTGTGCAAAATGTTTATATCACAGTC
WI-13967	103 A C AAATAAAAA	AAAAGACTAC	TTGTGTTTCA		AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAAACAAGATAAAATATGTCAATTCAGCAGTCATTTAAAAATAAAAGACTACAGATACAAGGAAATAAAAA/AJCACTTTTAGGAGATGAAAAACACAAA
WI-14408	60 T A G	GCAGACAC	TTAATTGTGA		TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGT/AJAAATAACAATGAGTTTTACACAATTAATAATTAACACATACTATTGGGATTTGTTGAATGA
WI-13683	47 C G ...				TTTTGTGTTAAGAACAGCATTTTGAATAAAACCTATCTGCCCATG/C/GJTTTACAGCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63 C T CGTCT	CACCATGGCA	CATTGAGATAA	AGCACATTAT	TTAGAAAAGTATAAAGCAACACAACTTTTGGGGAAGCACCATTGGCAGCTCCTTTGTGCTA/CJTTGTGATAAGTGTCTTATCTCAATGAAGCAACCCCA
WI-14635	22 G A ...				ACATGGCAGATACAGAGCTGT/CJG/AJCTTTGAAGACCACTGACCAGGAAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGGAGCGTTGAAGGGGTGACCAGCACATTGACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG CAGAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCACTGAAC TCAAGTCATC A	AAACTAAAC CTTTGTGCTA AAA	GTGGAATTTTAAAGCCATCAAAATTCCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCATCA[G/T]TTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73 T C	GCGTTTGACTT GTGCGG	TCCACACTGC OCC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTGGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCAGTGTGGACGGGAGGATTGCAACAGAGTTTCATACTG CAA
WI-12535	50 A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTTACAGTGTGACTAGGAGGGTTGAGGTGTAGATAT[T/C]TCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTTCTGTGTTTATCAGCTGAGAAGGGCAGTCTCGCCATC TTAAAGACCTGCGCTCC
WI-13805a	112 G A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAGGAAGGAAATTTTGGC CCCAGAAACCATGAGATTTGGTCAAAAAAGGCACACGGGAA[G/A]GGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	---	---	ACACAATATAATCCATT[T/C]GAGTGTATTAACCTATTGTTGTTAGAACCACCAAAAACTAC AAGAAAAATTTTCAAACCTTTTTTTTTCAGGCTGA
WI-14808	52 T A	ACCACCACA CTACCCGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT[A/J]AAAACTCTTAAC ATTGTGATGCGCTCTGCATCAATTTTAGAAAAACAAGAAAAACACAACACTGAAGGCCCATGTA
WI-14816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTAT[T/J]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71 G T	---	---	CCGTGTTTCAATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCAATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AACTGAACA TTTTAA	TCTAGAGCCGT CACATGGAT	CCGTGTTTCAATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTT[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGAATA CAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAAACCTGGGGATACAGCAGTAAAGAATACAAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28	T C	---	---	TC TT TG AG GG GA TAG AG GAC AG AG T G T T / C G T T G A T T T T C G T T C G G T T C A G T T G G T G T C A T T G G T T T T G T T T T G T C T A T T T T G C C C C A C C C T A T A A A A G C A G T G C C A C C C A G A G G C A G
			TGGTGACAG GAAATACCT 60 A T A A	TTTGTTGCTA CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAACCTAAATATGATGGTGGTGACACGGAAATACCTAAATATTTAA AGTTTGTAAGAGTAGCAACAAATTTGAGTATATACCTATACTATAAGTGATAGAGGATGATATGAAAAA GGCTATAAAGAGCTCCAAA
WI-14863	61	G A	---	---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14867	46	T C A	GACATTCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAACGTAAAAAGGAGGACATTCCTCAAGGCTCTCTAAACAT/C/GAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98	G A A	CCAAATTGAC AGATAATTCTGC	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCCTGATGATTTCTTTGTCAAAAAATGTTTGCCTGATTCTTAATCATGAAGAACAAT AGAAAAATCCAAATTGACAGATATTCTGCA/GA/JAATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAACAAACAAAA
WI-14898b	79	A C	---	---	TTTTGTACCTATCCCTGTTTCAAGTGCATGTACAGGAAGAGTTGTCTCATACATAAGTGCCACTAAGGAAA ACTTCTCCAT/CJAAGCTGCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTCATCT GCCTGTGTTCTGTCT
WI-14898a	50	A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCT AGTGGCACT	TTTTGTACCTATCCCTGTTTCAAGTGCATGTACAGGAAGAGTTGTCTCAT/C/JAGGTGCCACTAAGG AAAACTTTCTCCATAAAGCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCTGCATC TGCTGTGTTCTGTCT
WI-14907	48	G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/JATTTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCCATCAATCAGTGACTCTGCTGCAGAGGGGGCCACATG CAGCATGCTCACGTGTG
WI-14911	52	G A C	CCAATACATT CAGTTCTCTGGT	CAAACCAGGA AAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCAAGTTCTGCTG/GA/JAAGGTCCCTTTTC CTGGTTTGCAGACAGATACTTGTCTGTATCTCTACATGGCAGAGAAAGAGGAAGTAATCT
WI-14913	88	C A	---	---	CTGATGCTTTGACATCTGGGCAATTTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA/C/JCCTGCACGTGCACCTTTTATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCCT
WI-14914	66	G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCCTTGGTGTGCTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA/G C/GAATTTATTGTCTCTGGGCTGTGATGGCTTTACAGC
WI-14926	49	T C	---	---	GTTATTTTCAAAATGACACATCCAGATTTGAAATGGGCACCTAGCGAAT/C/JACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGTTTTCAAAATAAAAAATTTTCCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAAGATT OCAGCC	GCATCTTTATTACCACAGAAACTCATTTATGTCCCTTAATCATTTGTTTAAATATAATAAAGCATGTT TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTCCATCTATAGAAAAAGCACTAACCATC CATTAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCCCTTTCCACAGGAGGAGTCCCTCATGGATC/TGGCGGTATTG GTTGGTTGGTGATTGGGGAGCAAGGAGAGCAA
WI-14946	47 T C	TCAATCTGAAGGTGTCAAAGTGGTCTATTTGCCCCAGACATAACA/TCTCTCTAAATCATCTCTCTA GATCAGGGAGTCATAAGGACCAATTAAGGCTCATACACACAGTACTTTATGGAAAGGATT
WI-15987b	80 A G	ACATTAACACAGCACAAATTAAGGGGTCCCAACGAGGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTC/A/GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-15987a	32 C T	CACAAATAAA GGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGGTCCCA/C/TGAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAACCTCTCAGC
WI-14948	56 T C	AGGGAACCTG CTAAGTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTTATGCCGTTCTTCCAGGGAACAGGGAACCTGCTAACCTTGTACG/TCTCCAACA ACTGATGAAGATCATCTTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAG TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC/A/GJGTAATATACTG TTTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGG	AATGCATTAT TTGGGTTTT	GTGATTGATCTGTAATTATGGGATTATTTATCAACTCTAAATTTCCAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG/A/GJAAAAACCCCAATGAATGCATTTTCAGTTTCTCCAGGCTTTTGAACCTGC AGCAGAAAATTCAGGA
WI-14976	35 C T	GTTGATTGGCT TCGTTCAAAG AGC	TCAAACATAAT CTTCCATTCTA AGC	TATTTTAAATTGGTTGATTGCTTCGTTCAAAG/C/TGGCTTAGAATGGAAGATTTAGTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAGAAGATGCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACCTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT/GJTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCT	TGATTACATTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATTCAAACACCCTCTGCATTA AATGAAGCTGCAG/C/TJAGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72 T A	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCTTCTTGA TTTCC/T/ATTCAGTTTAGGCTCAAATGGGCTCTCCCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/G/ATGAAGTTTGTGCAGAACTAGAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACCT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTTTATACACAATACCTTCTGATGACCTATGAAATAA G/AJACAGGTAGGGAATATGTCCAGTGCAAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTATTACAGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTAGTATCTAAAACA/A/TJCAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCTTTAT ATTGGAATTTT T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAGAAACATTTCTACCTGAAGACTCCATGCAAGT CAAAATTCCTCGCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/TJ/CTCACAATACCATATACAACATACT TTCAATCACAACTCAAATATAAAATAACCTACAAAAATCACATTGC
WI-13712	40	A C TCTATTG	TTTACTTTGTT GTCATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGATACCCCTTTACTTTGTGTCTTTTTTATTCTATTG/A/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTTAAACAAAGACAGTGTGACATTATTTCAGGT
WI-13453	88	T A TC	AATGCACAA ATCTTGCTCT TC	TCAGATTTTTA CATCTCTTCT AGCA	TTTTTTTATTGCAATTTGAGTGTCTTTATTATATTGGGAATTGCAGTGATTAACATTTGTACAAAT GCACAAATCTTGCTCTCTT/TJ/ATJGCTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT/CJCATCTT ATTCACCAGAGCACACACACGACAGTAGAACAGTTCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A	GCAGAACCAATTAATAA/G/AJAATCTGCAAGTTTCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C	TGTAGTTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATCCCAGTATCATGTAC GCACTAAAAAAAT/CJGTGTGCTTGTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C CAGAGTGGC	TGAAGATTAA CCAGAGTGGC	AATTGTGTGGA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTACTCTATAAAACCAACCCCAACCTTCAATA TTACACTAATGAAGATTAAACCAGAGTCGC/A/CJCTCTTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTTCATTGAAGCTTTTGTJATACCT TACTATACTCTAGGCTATTGGAGTGTTCCCCAC

WI-15100	74 G A	TCCTATTCACAGCCAAAGAAATACCCAAATATTTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92 A T AATTACT	GTCAACCATGTT ATAATTTCTTT TAAGAC	TGGTACAGAAATGTTTAAATTACAGCAGGGCAGTGATCCAGTTAAATAAATAAATTTAAACCTTTATTTT CCCAATATATAAATTAATAAATTAA[A/T]GTCTTAAAGAAATAATAACATGGTGACAGCTTT
WI-12002c	89 T C	TCCTTAATTTTATCGGAATCCAGGACACAAACAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68 G A	TCCTTAATTTTATCGGAATCCAGGACACAAACAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30 C G GGACACAA	TGGTATTTGGG TGTTTTCTT	TCCTTAATTTTATCGGAATCCAGGACACAA[C/G]AAGAAAAACACCCAAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96 C T GTTCAGTAA	CCTGAATATGC AATTATTTATT ATGACA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACATTACATATAGAATTAACCTTTG TTCTGGAATGGAGCCCTAGTTGCAGTAA[C/T]GTGTCAATAAATAATTAATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37 C T AATGGGAA	TCAAGCGACCA CCAAAC	GCAAAAGCAAAGCTATGGAGGCCCTAAGGAATGGGA[C/T]GTGTGGTGGTGGCTGACTTGGT GCTTGTGTGCATGGAGCAGAAGTCTCTGCTGATGCAGGGGGCTCACATATTTTAACTGCACATAAT TTGGCAAACCTGTCATTG
WI-15153	40 A G GCATTGCA	AACCTCAGATA AGTGCAGTGT T	ATTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA[G/A]GACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTTCCTAA
WI-15215	84 G C TCAAATGGG	CCAAACAGGGGA AAAAGTCA	CCTTGTCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAATGGG[G/C]TGACTTTTCCCTGTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80 C T C	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGGCGATCATTTGGATGGAATGATTATGTGCACGAGCATTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATGCAAGGTTGGAGATATGCTAAAA
WI-15152	51 G A	AATTTGCTAGTGCAAATGGACCCAGAATTGGAAGGGCTATGTAACACAC[A/G]ATATGCACACCAC AGCCATGTCAGTGTACAGATCCTCTTGTCATTGCACTTCTTAAAAACACATCAAAGGCTGCA
WI-15123	55 C T TAGGATG	TGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTACTGGGAAGAAACAGACATGCAACACGAGATAAACAACAAAT

WI-15182	49 C A	GCACAACAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACGAGGCAAAATAC/ATGCTGGATTAAACCC ATGCTAATGGGTTAOCCTTATTAGTAATCATGGGTCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGCCCTGGC ACTATG	ACTTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTGGCACTATGTC/CTACTCTGCTGACGAGATAAGTTGGC ATATGGTTCAGATTGCTTGCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12801	42 T C	CATTATTGAG TATTCTTGCTT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGTAAATAGCCATTATTGAGTATCTTGCTTTGATT/CTGCTACGTAAAGCATGTAAGACT ACAACATTACGACCCCATCTCTCAAGAGGAAGTCTGTTATTTATGGAAAAACATTTTGTGTCATTGAGAT T
WI-14510	104 A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAACTGGCA	ATGTTGAGAGTAAATATGCCCTACATATTAGTGAAGTACACCCACAGATATTTTGGGGAGAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAAT/ATTTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATTAACACCATCATTT/CTGCTGAG TCCACAGATAAGGTCCTCCCGGAGAGGGGCTTCCCTCTTCTGCTGGTTGACGTTCCACGCGGAGT GAAGCCTTTTCTGGAATG
WI-12634	52 T C	GCATCATATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAATGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTT/CTGCTATTAGCTA TGTTTACAATTGTCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTATTCTCTGA
WI-15249	34 T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCCTGAAGGGCTTGACACAAAGTTCTAACTTT/CTTGTAAATCTCTGGCTTTCTGCTGGCTGG TGAGGAGGCACAGGCTGGGCTTCTAGGTATCCACTGGTGCCCGCATCTGTTCCCTCCACTCCCGCAG CCACATCTTCTGGCTCT
WI-12159	28 C T	AAGACACCGT GCAATGTC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACACCGTGCATAATGC/CTAAAGTGCACCTGAGGAGAGGGGCTGTGTGACTC CCAAACCCCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12648	41 A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTGGAATGCCCTAGTGGCATTAGGATGC/AGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCATGTTAGGTGCTTACTTGGATTATCTCACTTAAACCCACA
WI-12684	64 G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTAGTAACCATGCTGTAAACAGCTGTGC/G/ TCCATTTAGGCTTTGTTTCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75 G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAAGTGGAAACAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGAATGAGCTGGAGAAATTA TCTG
WI-15325	39 T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCATGTGGCTGGGAGGCT/CTTCACAATCATGGTGAAGGCAAAA GGCACATCTTACATGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATC/CTAACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G T A A A T	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTA AAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAAATTATAAATTTTAAATTTTATAATAAGTGTCTAATCGAGACATCACTGGGTATAATTGA TATTCTTTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAAGGAAAAAGA ACAAATTTTC/JCAAAGACTTGGGGAGTGAAGGACAGAGCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-15347	74	C T A A T T	GACTTCAAAG GAAAAGAACAA	TCACCTCCCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/JCCTGCACGTGCACCTTTCATATACAGATCA TTTATTGGCTGTCTCTGTAAATACAATGTGGTGAACAC/G/JCCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTCAAGGCACATAGGCTGATTAAATCAGTGG
WI-14546	95	C A G G A C T C A	GGACTGATA GATAGTAGA	AAGGTGCACGT GCAGG	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATCTCCATCTGTCTTGA/G/JGAGGGATCTTGGTGGCTTAACA
WI-15353	37	G A ...	CATCCCATCT GTCITGCA	CCGACCAAGAT CCCTCC	CCAGCTGGAGGTGGAATAATGCGGCAACCACAGAAAAACACACAGCTACACACAGGCTGCATT TGGCTTAT/C/JGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGATGTCT
WI-14580	100	G A G T C T T G C A	GGCTGCATT GGCTTA	GCCTTCTTTT TCAGGGCAC	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTTAAATATGTAT/C/JGTGCTCGTGATGTATTAATATCCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGACACAACTGACAGAAAGAGCAGGGA GACCAGACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACCCACA
WI-8039b	97	T C ...		---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACTACGCACATCACGAGTAAATACTG TTTGGTAAAACTTGTTCAGTTTAAATATGTATGTGCTCGTGATGTATTAATATCCTTCT TACCAGTCACTCCCTAAAGAACCAAGCTTAGGACTAGGACACAACTGACAGAAAGAGCAGGGA GACCAGACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCACCCACA
WI-8039a	87	T C ...		---	CACAACATTCAGAAGTTTTTCTGCATTGTCTTCTCTGATGTCTAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCAAGGTTTCTCCCTC/JA/JAGTATGGATTCTCTGATGATTAATA AGCCCGAATTCTGGCTAAAGGCTTTCCACATTCAAGACATTTGTAAGTTTTTCTCCAGTGTGGAC TCTCTGGTTTGCACAAGAATGGAACCTCGGCTGAATGCTTTCCACACT
WI-8044	107	C A ...		---	CTTACTACATGGGAACATCAATGCAACAAGTA/G/JAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8550	32	G A A T G C A A C A A G	GGGAACATCA ATGCAACAAG	AGTTTACAAAT T	TATTAGATAAAACCCCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAAGGACAGTT/JAGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGAGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG
WI-8057	87	T A ...		---	

WI-6192	91 A G	GACTGCTAAG GATTTAATTTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAATTTGGATG/GATTTTAATACITTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105 T A GAAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCTCACAAATACATTTCTCAAACCTCAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTCACATGGCAATGATAATAAAGAAAT/AJATGCAGACTACACTCTGAGGATAG AGCTCAAAGAGTAAACAAATGGAATTTGGAAAAATAGGAGTAA
WI-6213	164 C T	CATATGCTGCTTTATTTCTGTAAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCTACAAGAAATGTTAGTATGTTATGTCAATTACATGTTT ACTTTGATATTGTCTCATTACTATGTCT/TATATAAATGTAATAACAGTAAGTAGGTGATCC TGCATTTCAAGTAAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
WI-6217	131 C T	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGGTGGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCTGGCTGTGAGTGTGCTCAGGGCTTGACAAGCAGCTCATTTCAAG[GCT] GGCCACCATGGCCCTAGGGTGTCTCAAGTCCAGCAGCAATCATGGCTTCTCGTATATCTGATCC AC
WI-6238	175 G A	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTGTTTATGCTTTTTTTTTT TAGAAGGTATCTACATCTGCATTATTTACAGCCTTGTGGTATTACACAGCTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAATCTCTCAAAATTTG/GTTCAGAGCTTCAGGAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTATCCAGGAAGCAGCTTG
WI-6272	86 C T TAA	GCATTTATTCA GGGAAACTT	CTGTTTTTGA GAAGACAAAAG AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCATTTA TTCAAGGAAAACTTTAATTC/TTCTTTGTCTCTCCAAAAACAGCTGTCTGGAACACCTCAAAATTA GGGATGTTTCATCTAAACACCTTTACTGAACTTGATTCCTTGGCCAGAGGAGGCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAAATGAATACCTTGATGATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAGCTCTGTCTG[G/A]CTGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCTCGATTTCCTGCCAGCAGTCTTCTCTCTCATCTTCTTGCCCC TCTG
WI-6303	96 G A CTCTGTCTGC	CCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATTATTCCTTTTTCAGAGCTGTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTCAAGCCAGCGTGTGATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTGTC/TCTGTT CTTCCCTTACATCTTTTGGGGA
WI-6315b	193 C T	ATGCTTTTGCATGATTCTAATTATTCCTTTTTCAGAGCTGTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTCAAGCCAGCGTGTGATGCATCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTTC/JAGTGTCTCTGTT CTTCCCTTACATCTTTTGGGGA
WI-6315	187 T C	

WI-6375	28	A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[AG]TATCTTTTACAAAAAAGGTTAGAAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGTCCCTCCACCCCTATATTTAA[TA]GCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112	T A	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[AT]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTTATGCAACTGACAGTTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73	A T	CTAATATACTCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACATAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165	G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAGATGGGC TCCTGGAGTCCAAACAGGATGGACGTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCAACAACACAGCAAGCTAAACCTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195	C G	ATTGTAATTAATAATTTACATGGGCTATTTTAAAGGACATTGTGTAATGTTTCCACTTGTGTTTAAA [C/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68	C T	ATTGTAATTAATAATTTACATGGGCTATTTTAAAGGACATTGTGTAATGTTTCCACTTGTGTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42	G C	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATACTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAACACAGGAGCTCACAGCAGGGATGTAAGAGTTAATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75	T C GTCATA	TCITTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTCTTGTCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCATTCTCAAGCACAC T/C]ACCCAAACTTGAAGGTGATTGAACCCAAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGTTTATATTTTATGTTTGCCAAT
WI-6644	134	T C	TGCTAAACACCACCATTAATTAAGGAGAGTACTAGGAAAAAACTACCAAAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTATAGCTGGTCTGTGTATTAACCAAGAGCGGTATCTGG
WI-6690b	108	C T AGCCACAGC	CAGACTCTGG	TTGCAGTGTAT TAGCC	

WI-6690a	28	T C A G	AAACACCACC ATTATTAAGG	GCTGTGTTGG TAGTTTTTCT	TGCTAAACACCACCATTTAAGGAGAGTC/ACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGAAGGGCACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53	A G A C A C	CAACCCCAA AACATCACA	GTATAATAGTA TGAATAA	GATGTTTATGACACAGATCTTCCAAAGTAATCCAAACCCCAACATCACA/AG/AAATTATTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A G A	GCAATCTCCA AAACAAAGA	CCTTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAAAATCAGCTAGCACTAATCTTGACCAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTTTCAATTTAAACACATGGTAACCTCCAAGCATTTCT TCCAAAACAAAGAA/AG/AAACATTGGATAGTCACTTACAAGGAC
WI-6761	32	C A G	GATCTAACAG CTGCAGAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/C/ACTTCTTCCCTCCAGCTTTTGTGAACAAAAC AATTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTCAAGGTACAAGGTCTC
WI-6844	225	T C	---	---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGATCATCTTAAACAAAGGGTATTTCCCTCTTG GTATTTTCAAATGATGCATTATACAATAAACGAAGTTAGAACTTAAATGCACCCTGATTAAATTATG TAAACTGGTAATTTGTTTTAAAGCATAATAATTTGGTCCCTTCTCATAAATGGAAATTTAAA TATTTCTCTGATAGTCTGGAGTT/C/ATCATATGAGTAGTGCAAGGTGTG
WI-6824	112	A G	---	---	CGGTTTGTACACTTAATGGTTTTTTTTTAAAGGATTTTTTTCAGGCTTGTGCAGCAACATCAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA/AG/CACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGTCTTGAAGAGCTTACAGTCTAGGGATTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATTCATCCCTAGAGCTATTGTG
WI-6889	139	T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAGAGGCCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/T/C/JAGAATAATTAAAGCCACAAAGTGAAACTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216	T C	---	---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAAATATCTGATGAACCTTGATGAACGTGAA AAGAGGTCTCCTTAAACAAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCAGAAAACTTGGCTTCCCAAGGAATGTTTCTAATTTGGTTCAAAGCACACTGGTTCC CACTTTTACCACCTT/C/CATGACATGGACAATAGTACTACTCTTTCTAC
WI-9413	112	G C	---	---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTGGGTGGAGGATACCGCTGCTATTTCCAGATG/C/AGAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74	C T	---	---	AAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAAACTTTTCAGCAAGATCAAGTAGCCACGCT ACAGCCT/C/TTGGTGCATCTTAACCCCTCTCTCTTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTACAGTTTCAACAACACAGCCCGTG(G/T)GGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTGGCCGGAAGGTCTCTATTCTGTCCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTGCACGATGCAGTTCAGTGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT(G/J)ATAATTCCT TGTTAAATAAATGTTTATAAATGTTTATGAAGTCAATTACATTATCTTTTAAAAAAGTAAAAA TTTGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	GCTGGGA	AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT(G/C)ACACCCACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGTCTCACTATGTTGCCCGCTCTCAAAAACAAACCAACTAAC CAGGGTCTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT(G/C)JACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACACACCTGGTTA ATTTTTTAAATTTTGTAAAGATAGGTCTCACTATGTTGCCCGCTCTCAAAAACAAACCAACTAA C
WI-13119a	51	C G	---	---	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT(C/T)CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGCTTTT	GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA(J/C)AAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAAAAAGAAAGCCCAAGGTCAAGATATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAAGT AAA
WI-12988	36	C A	CTCAGTACAA	GTTT	TGCTATTCTATGACAGACACGTGAGACAAAATATCTTATTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCTGAGACTTTA(G/A)ATCTGCAAGGGGTTTAAATAT GCAAAATATCAGATATATTTCCATTTTAAACCCATATTTAAGTTTTCCATTTTCTTAATAGAAAATGA TAAAAATGTTTCCCAATAT
WI-13020a	108	G A	CTTT	CATTATTAAAC CCCTTGCAGA	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAGTCCA(J/G)TACAAAAAACAGCAATTTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTGTGTCCA
WI-12837	87	A G	AAAGTCCA	ATGCTGTTTTT	

L42611b	50 G C ...				GTCTCAGGCCCTTCTCTGGCTGCAGAGCGTCTTCTCAGGTTGCCTGTCG/CJCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTTAC
L42611	34 T C ...				GTCTCAGGCCCTTCTCTGGCTGCAGAGCGTCTTCTCAGGTTGCCTGTCGTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCCTCTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGTTAAATCAATTTAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/7]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ...				TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTAATA	CACCTACATTT CTGAATATTTA GACTCITT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTGAG AAATGTAAAGTGTGCGCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTTGCCAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTTAAAGACATTAACATGG CCTGGTG
WI-1231b	141 G A ...				TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACTTTAC ACATTGGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTTCATTAATTTCTT CTTTCACGTTATTCCTCACCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAAAATCCACTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGCC		GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTTATTTTAAATTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGAAGGCTGACAAATTTGGGCTTGATT

WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTT	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGCTGTGTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTT CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTTAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACT CTACACAATCT T	AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGTTGGAAAGGAGGACAGGA CTGTTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCTAACTGAGTACT/AJCAAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/TJGAACAGAGAGGTTTCATTGACTCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGTAA GCCAAGT	AACAAAACAGACACCCCTCGGCTTCTCTCACCAGTCCACATGGGTGCCAAACAATCCACATTCCCT ACATCTCCCACTGGGCTGCCCTCTCACAACTCACCA/AGJACTTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTGATTTAATCAACCTAGCCG/AJGCTGTCTATGTGGGATTAGAATAAAATA AACACAAAAATGAAAAACACAGATTGCTAACAAAGCAGATTCTTTTTTCAAGGCACACGCTAAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGCATTATTATGCAACCAATAAATCACTCTGTACAT/ATJCATTTATTGTATTTCATTATCACAAAAT TATGAGTGAGGATGATTGTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTGGAATCCATCACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTTGCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCCTGACCTGTTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGGGTTTTTGTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTTTTGTCTGCTTCTGTGCACTGAAG
WI-5381	178 A T	---	---	TTTATGCAAGAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCATCTCTATCCACGTGCAGAACTGGCAATTAGTTTTGTIA/TTTACTAAAAACACAAATGT TTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	---	---	CTATGATTCCATCTAGCAAAAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG/GAJATCGAAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCCAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCCTGTTTGT TAGGAA

WI-5791a	44 C G ---				CTATGTATCCATCTAGCAAAAAGCAAGACTATTTGGATAAGTTTC[G]ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---				CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C]TTATGAGCCAC ACTTCTCATTTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C]CTATGAGCCAC ACTTCTCATTTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406a	42 A G ---				CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGGAAAGGAAAGGAAAGAGAGGCAA GCCTTTTGAAGGAGCCCGAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTATGAGCCAC ACTTCTCATTTTCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT		CCATTCTCTTCTCCCTCCCTTTATTCCTCCCTGTTTTG[G]CJATTGAAAAATACTGGTT TTCTAACAGTGTCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATCA TGATCCGATCT		CCTGCTAATAATAATTTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTTT[A]TAGATCGGAT CATGAATTAGTCCAGGCTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG[C]TCTTAAACCATATTTTTGTTTA GAACTCTCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTCG	TGTCATTTATG CTGCAGTCG	TTACTCCAGG CTCCAAGTAT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A]GJA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5481a	29 G A AATTT	CCAATTTAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGCATCTGTTTTC AACTCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCAACAATTA
WI-5492	38 T C ---				TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCAT[C]CAAAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C ...				TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGTC[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACCCAGCCAAACAGCCTCACCTCTTCCTT CCTTGGTGCATTTACTCTTTACAC
WI-5546	40	C T A				CCTTATAACCCCAATACTTTTTCAGGTGAAAAAGGGAAAA[C]/JACCCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT TAGAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T				TGTTTGTCTGCACCTCCCCAACAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCGCCTTTTAGAGTC/JCCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T ...				TAA GTT GATT TAAACACTCTGTGCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACTGGTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]/JCCATTTTGAATAATGAGCTTTTGAATTTGTTTCCA ATG
WI-5573	58	C T				TCGGGTATTAGGATGGTTCACCTCGATGATGGGGTTCATAAGGAGGTGGGA[C]/JGACAC ATTACTCTCCAAGTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A ...				CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTATGCACGCTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTC[G/A] JTTTTGCCATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5850a	92	C T ...				CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCTCTATGCA[C]/JGCGTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCCTGTATATCAACAGAGAGAGGGTGG
WI-5612b	125	A T TTC				TGCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACAT/JACACAAATATCTTATTTCTGCTG TCACACTAATTTGCAAGCAATCAATGATTGACTATTATGAGCATCGTGTCAATTC/JCAGTGTT TTAGGTTTCTCAAGAGAAATATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A ...				TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACAT/JACACAAATATCTTATTTCTGCTG CTGTACACTAATTTGCAAGCAATCAATGATTGACTATTATGAGCATCGTGTCAATTCACAGTGTT TTAGGTTTCTCAAGAGAAATATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5636	26	A C				TGAGAGCCCAATTTTATCCGCAATAAA/JCJTCCCAAAAGTCCCTCGATGGAGGCATTTTCAGAAATCGGG GCAGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ...			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAATTAAC[G]AAATATAATTTTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCITCA GAGAAGACAGACAACTAAATAATTCAGG
WI-5865b	99 T A ...			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAATTTAAACAAATATAATTTTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCITCA GAGAAGACAGACAACTAAATAATTCAGG
WI-5865	165 T A ...			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGTCTATCAAAAATTAACAAATATAATTTTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGTTA]CCAGTCTCCATCTTCAAAAGGTCACAGTCCITC AGAGAAGACAGACAACTAAATAATTCAGG
WI-5874	76 T G ACAGAAAA ATAATATTAT	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTATTAGTTGTTAAATTTTGGTATTTTCATAGCATGGATAATATATACAGAA AAAAAATTT/GTACATATCAATGACTGAACTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCGAGCTTCAGCCTCTCAGTTTTTCCATC]A/TTTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTATTTCAACTCTCATCTGCTGATTGGATGTAGTCATAAAATATGGGTGATTC AGAAAAATAGTAAATG
WI-5752	36 A T TTTTCCATC	CAGCCTCTCAG AGAGTAAAT	GACAGAAAA AGAGTAAAT	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAAT]C/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAAGCCAGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760b	61 C G	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAAGCCGAGTTTTCGATTACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAAACGAAAGCCAGTTTTCCGATTACACAGTTAGTTGCTGTT
WI-5760	187 G A	AATATCTGGCCTTTTCTCTTAGGAGGAGATTTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCACCTCTCACTATTGAGAAGCTAAAGTGTAAGACTACTCATTTCTCAGTCTTCCITGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCCCACTTCACATTCAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGT]C/T]TTGCTGTCGCGTATCTGCTCCAATCAACCATCCACTTTATTTCCCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148 C T	

WI-5967	165 C T ...				GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCCCACTTCACATTCCAGCAGATATT CTTTCATGGGTATTTGCCCAAGTCATGAGGAGATGCATGTAATGTGATCATTTCAAGAGGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TGTGCTCCAATCACCCATCCACTTTATTTCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ...				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTCAGCAAACTTGTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAACCCCA GAACAGTG	CTC	GACTCTGTCTCAAGAAAAAAAATTGAAATTAATAATTAAAGCACTTCTTAATTAAGCAT CTACAAGGTACTTAT/C/C/CACTGTTCTGGGTTTCAATCCTCTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAACACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAATTTGTCTTTT
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT	TTGTTGAAAT GTGTGGTACTT CT		ATAGGACAGTTTTTCTTCCAATGACTTATCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGCCAGGCTATGCCAGGTGGGATTATTTACGGTCACTGGTAATATGCATGTAAAGACTA TTTTACTGGCCTTCTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGCAATACAG CAGTTGTCATGTCCCTCTGGTACTAGAATATAGTCTTTATAGAATATGTGTTAGAATAAAGCCACA AATTATCTATAAAACAACA/C/JAAGGAACGAGGCTCAAAAGTGAACAACCGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-7466c	141 G A TTTGTCTGG	TTTTCACAGTC	AGTCGCATGCC AATTTATAAT		GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATTCITTTGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/C/JATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTACAGTCTT CCTGG/G/A/ATAATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA	TGCTTTTATG ATAACTAGTTC ACTGAA		GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATTCITTTGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/C/JATTCACTGAACTAGTTATCATAAAGACATGCAAAAACCTTTTACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTTCCCTT
WI-9814	104 C A ...				TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT/C/JATTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGTGCTTTTTCATATTGATTCTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9720b	55 A G ...				CCTCTAACAAAGAAACCTTGACTTCTCCTCACTCAAAATACCCTTCTCTATAATTTTJAGIAGTAACCA AAATATCTCTTCAATAAATTAATCTTTTAATTAGAAGAGCAACAGTGTAGAGGTAGTACATTCA CCAAC

WI-9720a	47 A G ---	---	---	CCTCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTA/GJATAATTTAAGTAACCA AAATATTCCTTCAAATAAAATTAATCTTTTAATTAGAAGAAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	---	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGCTGCACACCTTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTGCTA/TJGAGGATTAG TAAGATCTCTTTCTAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTTAGTTGCATT TAAGAAATGCCAGTCTTTTGCTGTCATCATCTTTGAACATTAATCCACATG
WI-9748	74 C G ---	---	---	CCACTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTTCTAATTTTTATATGTTTACCCTTT GTCATT/C/GJTCAGACCAAGTACATGTTTTACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGTCAGATTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTCT/CJATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAATATTGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---	---	---	AGGGCCTTCACAGATCCGTGAGCTCAACACTGCCTCCT/CJAGTGAGCCTGTGAACCCACCCAAAGAC GGCTGGTCATCAGTGTCATCTCTCTTTCCGGACAACATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAAATAATCTTATTAGGCCAAATCCAAT GTGCTGAATATCTGCCAAGCATGTCTTCTACACAAAAGGATTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAAATATTGAGATCTCCCCAAATGTCATGATCTTGTTCTCAACATCCTATTTTCTCAAAC ATTTATAGCCTGT/CJ/JAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAAATATTGAGATCTCCCCAAATGTCATGATCTTGTTCTCAACATCCTATTTTCTCAAAC ATTTATAGCCTGT/JA/JAAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAAATTAGCATCTTATTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGAAGTGGCAGGGGGAGTTGAGACA/C/JAGCCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATAA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCA/C/JACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGAAGTGGCAGGGGGAGTTGAGACAAGCAAGAAAAGCC TGATATTAAGAGGCACCTTGCAATAA
WI-9983	146 C T ---	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTCTTGTCTTGA TTCCCCAAACCCAAAGTTCTACCCCAATCTGATCAATGTGACTAGGTATGGCTGGTCAGGGTAA AGCATTATGA/C/JAGACACAAAAGACAAAAGAGGTTAAAGTTGCTGCTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T	ATCT	TGATGTAATGC TATGTAGCAA	TGATTACTGT GCTTAGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGTATTTATGTGCTATAAATCAATGGTCTA ACATTCAAATAAGATCTTTTGCCTCTCTGCTCAGATGCTTTCAATGATGATTAATGCTATGTAGCAAAT CTA/ATTTCCCTTAAGCACAGTAATCAAGGCCCTTACCCCA
WI-10020b	122	T A	TTT	GGGAGAAAAG AAATCATGAC	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTT/AJAAAAATACC AGACTAATGATTAATAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C	ATAAATT	TGTCATCTTGA CTCGTATTAA	AAATTCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAT/CJGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAATAATAAATTAAACAGTCTAGGGTTCGGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10084b	170	C T	TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCITTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/C/TAATACTGGCTTCAGAAAGGTTAGGTGTT T
WI-10084a	54	C A	CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG/C/AJATTATAATA AATATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C	CAAACCTCT	TCTCCTGTCCC CAAACCTCT	ATCTTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCTCAAACTCTTAT/CJTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCATGCCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTCACCTTAGAACATAGTTTATTCCTTTA/TAACCATAGGGGTGTGGCTTATCT TTTACCCTGGCATGGCTTAGGTCTGTTTATAAATTTGGTATCTTTTGGCACAAGAGTGTGTTCTGAC AGTCTTATGATCTCTATTTTAACTTAACACTGGTCAGATGTGTTTAAACTTGTGAACCTGCAGC
WI-10316	104	T C	CTCTT	CTGTTGATTTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTATCCAGTCAACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATCTCTTAT/CJTAACCTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C T	AGTGAGTTGTGCACAAATTTGGAGACATTTGTGACCCCAACTTAAACACTTCTCCACAC/C/TAAC AAAGTTAACTTCACTTACCAGGTGATGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGGCTTGTT	CAAGATAATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAAGGCTTGTT[C]/CTACCCCTCTTAGAGAATAAATAATATATCTT GAGATAGGAGGAGCAGCCTGAGACAGCTGGGTTTGTTCTACCCACTGGAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGOCCTTCAGGG T
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTTCTCTGTCTCAGGTATGACTCCCA[AG]/GTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGTCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTTCATATT TTCCAAATTATTAATACTAGAAATTTACCAACAGAAATTTTTTAACATTTTAAGTTACCCAGAGCTTT CTAATAGCAAA/CJAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTTCATATT TTCCAAATTATTAATA/CJTAGAAATTTTACCACACAGAAATTTTTTAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGGTGCTCAAT AAATATTATT CTTT	AAAATTCGTGT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCCTGACTTAGCGGGTGCTCAATAAATAATTATCTTTTTTCATATT ATTTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTTTAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	TACTTTA C	CAAACCTCAA AAATCCAACA ATTGCTTTAAG GTCAAGGCTTT C	CGTTGGGAATATTTCTATCTCACCTAAATATG[C]/AGTGATTAAATATACATTTTAACAAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTCTTTTCTTTTCTTAATA AAAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	AATTATG CACAATGTA ACAAGAAATTG ATCC	GCAATTTGAAG TTTGTTAAAT GTAT	GTTGGAACTCCAGTATCATTTCCCTCAAAACCGCTTAAATCACAATCACTTTTCTTCTCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTACAAGAAATGATCCTAT[C]/ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-2616	125 T C	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTTCA TTTGAGGTTTT T	TGACTCAAGGAAACACACACAAAAAGTTTCCACCAAGTGAATTTATGACCAAAATGAGA[C]/TAAAT TTGTTAAAAAAAACCTCAAAATGAAGAGACAAATATAGTTCAAAGATTTCAGTTCAATATTGT
WI-11163	58 C T	ACCTACAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTA GAATCCATTTTGTCTTTTGGCCAGCATTTCCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGTACTATTCACCCCATGGGGTCAAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTTGAAAACC
WI-10656	59 T G	

WI-1169b	154	T G T T T T	T T A C C A A G A G T T T T C A T T C A A T A T A A	C T A A C T T A A A A A T C C T C A T T C A A A T A T A A	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A T T T A A G C C T A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A G A G C A G A C A T / G / J T T A T C A T G T G T C T G A T A A T T T T T A T A T T T T G A A T G A G G A T T T T T A A G T T A G C A T
WI-1168a	95	A G T T G A A A A	A A T A A G T G A A A G T A A C T G A C T A C I T T	A A A C T C T T G G T T A A A A A G C A C T A C I T T	C A G C A T A G A G G C T G T T A G T G A C C T T G A G T T A G A T T T T C T A T C G A G A A A G C A A T A A G T G A A A G T A A C T G A C T T G A A A A A A A A A A T T A A G C C T A / G / A A G T A G T G C T T T T A A C C A A G A G T T T T C A T T C T T T T T T T T A A A A A A A G A G C A G A C A T T T A T C A T G T G T C T G A T A A T T T T T A T A T T T T G A A T G A G A T T T T T A A G T T A G C A T
WI-10685	25	A G ---	---	---	C A A G T G C T T G G A C C T T G G A T A G G T C / A / G A C C G G C T G A A G G T T G G A C A G T T G T T G G T T A G G T T G G A G A C C A A A A T T C A G T C A T C C T G T A A T A T A G A T C T T G T C C T T T G G G T T A C C A C T A G G G T C A C T A A A G A G A G A T G G G A G A C A G T C T C A A T C T T G T C T A A A T T C C A A A T A G C C A T G G G T T G G A C A A A A T A C A A G G T A G T G T C T C T A C T T T A A T G G G C A T A
WI-10686	133	C T A A G G	T G C C C C T G T C A A G G	C A A T C T C T A A A T T C A T G T G T A G A C A C A	A A T A A C C T G T G G C A C A T A A G G C A A A T A C T G A G C C C A C A G A G T G T T T T A T G T T A A T A T T A T G A A A A A A G T C A A G A G A C A A G A T A T A G T T C T G T A G A A T A C T T G A A A T C T G A T G C C C T G T C C A A G G C / T T G T G T C T A C A C A T G A A T T A G A G A T T G A A T G A A A A T G G C A A A A T T C A G A A A A G G G
WI-11175	77	T A A	A A A T G A T T C T T T C T G C T C A A G	C T G T T C T C A C A T T C T T T T T G A A A A	G G T A G G A T A T T C T A G A A T G C C A C T T T A C A G C C A C T G A A A T A T A T T G C C T C C C A A A T G A T T C T T T C T G C T C A A A G A G T / A / T T T T T T A A G T T A T C T A C T A T T A T A T T C T G C T T T T T C A A A A A G A A T G T G A G A A C A G T A C A A A A T G T T C A G T A T A G C A A A T T A A A A T T A A T T A A A A G T A A G A A A A A A G A G C C A A T T T G G C C
WI-10694	144	A G T A T G A G T T T C	T G C A A A T G C T T T A T G A G T T T C T G A A T T C A T C C A G A A A A A C A G	G G C A T T T T G T A A A G G A G G A A A T C T C T T T T C T C T C T T G T T G T C A T T C	T A G A G A G T C T T T C A G T T T C A G G T T G A G G G T G G T G A G G T G A G A T T C A C T T C T T A G A A G C A C T G G C T A T G T A C A G A A A G A T A A A C T G A G A A A C T C A G T T C T A A A G T T C A G T C T T T G C A A A T G C T T T A T G A G T T T C / A / G / J T T C C T C C T T T A C A A A A T G C C A T C A A T T C C T C A A G G A A A A A A A A A A A A G C T T T C T T
WI-2716	23	T C C	T G A A T T C A T C C A G A A A A A C A G	T C T C T T T T C T C T C T T G T T G T C A T T C	G T G A A T T C A T C C A G A A A A C A G C T / C / G A A T G A C A C A A G A G A G A A A A G A G A A T A A A G G T T T T G T A T A C G A C A A G T G G C T C A A G C A A T T T T C T G T C C C A G T G C A T G G A G C A G T G C A G G C C C A A C T C T G T C A T T A A G T G T T T T A G A A C A G A C A C C T C A G T C A C A C A A A G T T T C T T G T A T G T G C C C A C C A T A A C A G T T A C T G G A G G A T G A C T C T C A A G G C C A T T C T A G T / C / G G C T G C T G G C A G T G C T T T T C A G C C T G C T G C C C A T A C T A A
WI-10721	40	A G C T T G C C A	T G G C T C T G C T A C T C A	G A A A C T C C C A C A T A A A T A A A T C T C A	C A A C C A A T T C A G A T T A A T T T T G G C T C T G C T A C T T G C C A / A / G A T G A G A T T A T T A T G T G G A G A T T T C T G A A G A T T C C C A T G G T A A A T A G A T T C C T C T C C C T G C T T A G G T T T G A A G A A G T T G A A T C T G A G C C T G C T G C C C A T A C T A A

WI-11204b	88 T C	GCACAGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTACCTTTT/CJATTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA TACCTTT	TGATCACTTAA AATGTACATAA	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTT/AJCACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAGTGAT CAAAAAATTTTAATTGGGAAGAGATTAGTGAATCAGAAAAAATAGTCTGAGGAAAAATTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGCTTC CTTTAA	AAGAACAATG CATAACAGAA	ACATGTAATTTCTTTAGTGGTCAAGCTTCCCTTACCCCAAGAAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACCT/CJATTTAAAGTTCTGTATGCATTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTCTATAAAGAAATACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTC/A/TCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGGTGAATTTGAATCCACACATGGA ATAAGTCTA
WI-11215	68 C T	GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTTCCAGATTTATTTTAGT [C/T]ATTTTCTCTATAATTTCTTTGTAAGTATGATTTCTATAAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATCCACCATGT TTT
WI-11219b	89 G A AGAGAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA[G/A]AGAAAAAGTGTAGAAAAATAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11219a	18 G A	ATGAAAAATGCATTAGAAG[G/A]AATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
WI-11222b	136 G A GCCTGG	CATACCACCTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G[G/A]TCACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTCACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTG	AGCCACAGTGAATCATTTACACTA/C/TGAAATCAGCAATGCTAAATTTGGGCTTTGGATTT TGTTTTGTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCAGCTGCGG CTGGTCACAACTGGCTACCAGGAGAACTGACACAGACTTGGTAATGCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCCATATTAAATTCATTACACTC/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCTGGCAGGATAATCATTTGTTATCATTAGACATTGCA GGAACCACTATGGATGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165 A C ---		---	TTGCATGCATTTATACGAAAGGAAATAAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/A/C/GACATAGTTGCTAAGGATATTCACAAATATAT TTCATGA
WI-10778	62 A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/G/G TCCATCTCTGATGTACACAGCAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21 C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TGGGACACACTGCTCTAGACC/C/TTCCCAGGTCCTCAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGATCAGGGCCTAGTCTCTCTGGGACAGTGAAGGGCCACCAAC
WI-10810	58 C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAACCCCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGCTTTGTAGCAAGAGAGGAAAGCATCTTCATGGCAGGAATTC/T/CATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAAAGAGAAATGATGA
WI-10828	23 T C ---		---	GGACCAACACAGAAATTACTTGGCA/T/CJAGGGTTTCTTAAACATATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91 G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGAAATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC/G/C/JTTCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGITCGG
WI-10834	96 C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTCCCAAGACCATTAACAAGATTTAATAGTTAAAGCCAAACTATA AAGAAATTAACGTTCAAAAGTGTGTTAAT/C/TJCTTAATACCAATTTATAGGCCACCAATTAACCT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C ---		---	GGATGATGTTCTGTGGTCCCTTTA/T/CJAAAGCCTCTTGATCCCAATGTGTAATATTTTATTCT TGGTATTTCTCGCTTACCATAGTCACCTGTCAAGTGTCCACCCCT

WI-2296	81 A G	TGTTACTTTGA TTCCTTGCTCT	GCAATCAGAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAAATAGTTGTTACTTTGA TTCCTTGCTCTGACIAGCAGITAGCTGTGTGATTTGCAGAGGTTACATTTGTTTGTG
WI-2300	77 G T	GGCAGAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCCCTTTATTTGAGCGGGGAGGTGGTAGGCACAGAAGC CAGTCATACIGTGTGCTTTAAATTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55 G T	GTCCTTGTTCTT COCAGCTTCT	CAAAGATTGAC AGCCACAC	CAATGATCCCCCAACATTTCCAGGGAAAGGTCTGGTCTTGTCTCCAGCTCTTGTTGGTGGCT GTCAATCTTTGACATTTCCCTTGCTTGACGCTGTATAATCCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGGTGTCTGTG
WI-2395	122 A C	GAACATATTT GTAGAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAATATCATAATAACTTGGTTTAC TGAAATCTGAAAACCTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAAIACIOTGAATTC AGAATAAATAGAAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTAGTAACAATCTTTA CATTTACAAAAACCCA
WI-2437c	192 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGIGIAGCTGTG GTGCCAAGGACGCAATTATG
WI-2437b	179 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACIIGIACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2437a	128 G A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGIGIOTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTCCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTGIGIAGTGAGACCAATAGCAGAGTTGTACCTGCAGAACT
WI-1358	123 T C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAAACAT G	CTGTAACCTACACACATCCTCCTGTACCTCTAGGTTACTTGTATAACAAACACAAATGTAATGCT ACATAAATAATGTACATACTATATTGTTTAGGAAATAATGACAAGAAAAAGCCITCIGTACAT GTTTGGTACAGTTGTACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTATCCACAG AAACCACGAATG
WI-2886	46 C A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGAGAAAGIACIACAGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGAGAAAGAAACAGAGGAGCGTT

WI-2906b	77 T A	---	---	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGGAACCTTGCCTGGAATGCTC TTTCCCTGT/A/GAGGCTTGTCTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50 A C	GACACCTTCAT TCTTGCTGG	AGAGCATTCOA GGCAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATCTTCTGCTGG/A/CJACTTTGCCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTTGTGACCAACAAA TACTCCTCATCTCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCTAAAT TAGATTTCCACCCCCAGCACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTTCCATCTGTCTTCCA/C/TJAGAGATCTAGGGTGTCTTTGGAACC ACCTTGG
WI-1736	175 C T	---	---	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTCTGGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTTATTAACATGGTA CA/GA/JACAACCTCAGTTTAAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACATCATG TGA
WI-1851	136 G A	GCATTGAATT AACTATAGAT GTGTTAAGTA	CACTAGCAATG TTAAACTGAAG TTG	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTAGCACCCCAACACAGAGACCCCG/GA/JT GAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGGCTGGTCATAGTAGACACT ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCCCCCCCGGATTATTTTACT TAAGGGTTTAGCAAAATCACCTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTCTGTTTTGTTTTCTCCCTTCTTAAAGAGATAGTC/GA/JCCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
WI-3000	62 G A	CCCAAAACAC AGAGACCCC	ATTGACTAAGA CTCA	ACAACACAGCAAAATTCACACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-1754	177 G A	AAATTC AAC ACAGATCTAT TAGATTC	TGTGATAGTTT TGAGATGGGTG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGCAACTTGGCGCAGCAGAGAGGGAAG AAGTTGAGACCGTTGGGTAGGATAAGTGATCCAAACCCCTTGTAGGGCAGGTGGTGAGTGGGCAG ATAAAGA/GA/JCCAAGCCCTAGTTTGAAGTACACTGTGGGGATTCAAAG
WI-3208	140 G A	GTGGAGTGGC AGATAAAGA	TCACTCAAACT AGGCTTGG	ACTCCACCAACAGTTTGTGAGCCCAACCCCTGCATGGTCTTTCTCTGTCTG/TJTTTACATCATTTGCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-1775	47 C T	CCTGCATGGTC TTTTCTCTG	ATGACAATGAT GTAAA	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCCTTACAT/GA/JCAAATGCTC CTTTTAAGTCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCTTAGGA
WI-3402	55 G A	AGCATATTCA TTGATTTCTT ACAT	GAGGACTTAA AAGGAGCATTT G	



WI-3416	33 C T	CCAAGTTGTA GCATTGAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCAAGTTGTAGCATTGAGAGTCTC/TCTCTTAGAGGTAGTTGCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCTCAAAACAAAGTGACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGTCTACCTCTGACGCAACATAATTAATCCATTGCTTAAAGAGACAGG
WI-3453	70 C T	TTCTTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCCTACAACAACAGAAATTAACAAATGAAATCAGTACTCTTCTTAGGCCCATCAGAG AATCTGAGGTATGAGGAAATGATGCCATGTGAATGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 G A	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACCTTAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACATGATGAGGTGGTGGGAGAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACCTTAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACATGATGAGGTGGTGGGAGAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGTCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAATAAACCAATAAGAAATGGTGGAAATAAACGGGAGAGACCTGGG TTTCTGGATGTCTCTTGGAGGACAGGGTCACCCAC
WI-3600b	146 G C	GGTTCTAAC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG TAAACATCTGCTATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACTGGATGAGGTACAAA
WI-3678	125 G T	TAAATCATGCTTATTTTACAAAGGTAATCCACTCACAATAGGCAATTGATGTATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGACCTTGTCTTTTGG ATAGATGTTGATAGGAGATGGGTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAACTCACTGAATGAGTCCAAAGCCCTTATGCTTAC
WI-3687	67 A C	AAAGCGATGTTGAGATACCACTCCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T(A/C)AAAAAACTACTATAGTTTATGAAAAATGACCTCCAAAAATTCAGAGAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAACTCTCTGTCATCTTAACCTTGAAGTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA AAAAAC	GGCTCACCAT CATTGTTTT	TCTAAATGTGAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACTT(C)ACACCGGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCCTTATTATTAATGAAAA GATCTTGGGCAATTAACCT

WI-1819	51 C T	---	---	---	GAAAAAGCAGGAAGCCAGGACGACAAACTTTTGA AAAAGTCTTT CAGCAC[C/T]TTCGTGGATCCGG AATTTAGTGTGATTTGGCAGGCAATCGGGGTAAACATGTTCCAGTGTTTTAACTTGCACAGAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAATGTGGAAAAA AAAAAGGGTGGTAAC TGTT AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116 G A	---	---	---	GGCCTATTCACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGCTCTG[C/GA]GCCCCAGGATAAAAGCA GGCA
WI-3867	49 T C C A A	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG	---	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAAACAAAAGACACAGT CATTAAGTGGAGAAGCCAGCATCTTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25 A C G	TTTGAAGCA	TCGTGGGTGC CTCTCC	---	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCCGACGACACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAGGTGAGGAAGAGCAAGGGTTGCTGGCCACT
WI-3901	114 A G	---	---	---	GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGCTGTCTTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCCTGAACCTCGGCTTCTCACCTGACAAGTG[G/A]GTATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99 C T G C	TGATCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	---	CTGAGGAGATTGATGCTACTTTACCTGAGGAAACTTTTATTACCTCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTCTCAAGACTCACAG[C/T]ACCATCTCTTCACTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGGTACAAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33 G A A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	---	CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTTCTGTATTGCTGTTCACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAAGGCTC
WI-4091	84 A T	TTGAGGTCTTA GTCAATTGCATG	TGAGTTCCCTAT TAAGTGACAAT ATTGT	---	TAATTACAAATTGCTCTGTTTGTGCATTTATTGCTTCTCTTATGTAAACACAATCACCACAATTGAGG TCTTAGTTCATTGCATG[A/T]TGATAACAATAATTGTCACTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117 A G	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	---	TCCTCTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTAGGTGGCTCTAAGATGGTAATT ATCTGTCCAAAGTTTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32 A G	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTCAGA	---	CGTTGCTGGTGAGAGTCAAAATTGATACAAAACA[A/G]TCTGAAAAATCTGTTTGGCAATCTATTAAAGG CAAAATATACCAGCAGTGTGGTCTAGCAATTTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCA ATCATGATG	ATGCCTCGATATACTTTCCAAATGACTAGTATGAATAAGCACGTAATAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCCCTTTCCAAATTTACTACAAATTTGATTGTCACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTTG	GCCATGAGCACAGAGGCTGAAACCACCTCCCAAGTTAGTCAATATAAAAAA/C/CACACACATATTG TTATACCTAATCAACATATAATGTTATAGATTAAACAGTCCACAGCAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCCGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCCTG/C/TGGTCTGTTCCCTGTTCTTCAATGTTCAACTGCTTGAT CTGTGCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
WI-4250b	117 A G	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGGGGTGGGAAGGATCCTGTAAAGG/C/GTAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCTTCCAC	TAAGTGCATTAACTGTACAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTTGTGAACAGG/C/TGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCAT CACCT	AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGGAAAGTCCCATCCCTCTGATACCTTGGTGGTCTCCCCATCACCT IG/C/CCTTACACAACCTTGAAGTAGGCCCATCCAAACACTGGTCAGAAAGATACTGTGCGAC
WI-4256	57 C T	ACAGCCTCTTCAATGGCACAATCAAAAGCACCAGTAAAGCAGAGGCAAAATCTGG/C/TCTCAC CATTTGAAAAGTCTTCTGAAGGATAAGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4325b	71 C T	AGTTCACTGCCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACAGCCAC GATG/C/TTACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	AGTTCACTGCCCTAGATGAGTAGACCATGTTGCTTTTAAATGACTGTCATGGCAGGAC/C/TGGAAA TGGGATGCTACTATAGATAATCTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACAGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	TGGGCAGAAAGTCCGGTATGGCAAGTCAGGGTGGTTAACTGGATGCCACTTCTGCCCTGTACCTTCT CTAGACTTTGAOCCCTGCAAGGAGATCCCTGGCTCTGAGTTTATCATCTCCACCTCCAGCCAG GGCCTGTATCTGTTCCAGGCC/C/G/GAATGCTACGGCTCACAACCTGTGGGAGGTAGGAATGACGA G
WI-1936	117 T C	CCAGTCTAGGCTGCAAGGACTTCAATCTGGGGCAAGTCTGTTGTTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCAGGGTACTTGTATCACCT/C/CTCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAGACTCCTTACTCCACTTGTAGAAAAGGAGAGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGGGA

WI-5204	54 C T	TAGATTTTGATTGATGACAAATAGGGAAGCCCTTGTAAATGGGTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGCGCAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTCGC		TTTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTTCTTT		CCCTGAAATGTCTTGTCTCTCTCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTAAATTAACCTGTATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAAT	TTTCCCTGTTAT GCATGAACCTTG		ACACATTTTCATTTTGTCTTAAAGTTGAATTTTTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTTGGGSCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT	TTTGACCTTC ACCAATTTC A		CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAAATTATCCTTC[C/G]TGAAATTTGGTGAAA GGTCAAAGAAATGAAATCCCACTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75 G A		CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA GAGTGAATAA	GGTGAAGATT ACTAACTGTTT TCCTT		CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAA		GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCAATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T C G A G T	CAGTGGTGAG CTATCAITCTG	CCATGTCAGCA GCTTG		GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]AAGGCTGCTGACATGGTCAATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCAITCTG	TTCTAAAAATA ACACTTCCTGA AAAA		TGAGAGAGTTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTCTTTTATATCCTATGATTATTTTCAGGAAGTGTTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGTGGCTGGACAAGATGGGCTTAGGATCATTTT

WI-4540	110 A G C A T C C	GCACCATGTGG	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAATAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC/A/GJTGATGGCTGCAATTGTCCAGTC AAATGAGACAACCTCCTAT
WI-4582	226 T C ---	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACCTTATCCTGTACACA AATAACTTTATGGGAGACAGCATTGTAAITCAATCAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/C/CCTCCTTGCTAGAAACCATTTGAT
WI-1985	105 G C A G	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCTCT	CAAAGGTAGTTTAACCTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAG/GCJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCACACAGATGTGGAGTCATTTATTTGGTGGTATGACAGT CATGG
WI-5248b	99 C T T T G	CACTGTTTCT ATTGACCGTAC	AGAAAAGAG AAGAAGGGAA AAA	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/C/JTCTTTGCTTTTTTTTCCCTCTCTCTTTTCTG CCCTCTTTTAACATAT
WI-5248a	38 G C C T A C G T G T T	AGTTTGTGCTG CTACGTTGT	TTTTAATTTTC TGGGGTTCCT	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCCTAC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTCTTTTCCCTCTCTCTTTTCTG CCCTCTTTTAACATAT
WI-4596	69 T A A G C A C T G T G A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTGCTGAAGCAAGAACACTGTGA CT/A/CATTATTAGGCCCATCTCTGCTGCTGAAGCCTGCTACAGCAATTTGTACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTGACAAGATTCTCCTTTTAAACA
WI-5252	119 A C ---	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTGCTTT/A/CJTACCATGTACA TATTATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTAATGCCTA/A/GJC CAAGTAGACAACCTTAAGCACTAAGGCAGAAATGAAAGTTTCTCTCTTGTCAATTAAGTCTCTATTCA ATTACCATTTATCGGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A G C A A A G A G G	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATCGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAGAGG/C/AJCTTTCACTGCTCCCTGGTGGTTTTTCAGTAACCTGCAACATGCTTTGGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATCCACTCCTAGGTATGCACCCTAAACATGGGTG GCAAT
WI-4649	50 C T T T C C G A A T G	GAGACCATCT TTCCGAATG	TGACTAGGTG TACTTACAAGA AATCATC	TCACGTGTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATG/C/JGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGCTACCTGAATTTGTTATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A G G T C T C T T	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTGG G	AACTGTGTGGTATGTTGTTGTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCAATAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAACCAAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACACTTCAGTAACGTT
WI-4677	82	T C A A A	TCCAAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTGACATTTTGGAAAAAATTTGCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C]AAGTTGAATAATGACACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---		---	ATGATGTCATCATGAGGAATTTCTGTAGAAAAATTTTCCACTGGCAATTTGATTCAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G A A A C A C A C A C	TGCACTATGG AACACACAC	AATATGGAATC TGCATTGAGTT G	CTTCCCATTTCTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTATTATTTG TGCACATATGGAACACACACAC[G/A]CAACTGAATGCAGATTCCATATTGAATCTGGGAAATCAGTGA AAG
WI-2020	145	C A ---		---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGATTGTCA TAAAGGTCAAGTAAATCACTTTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACACGACGTGTTGTCTAAAAAATATGATAGTTCTTCTCTCTGTCACCC GCAATGAAAAGGAGTT
WI-2028	176	T C C T G T C T C A T C	TGTTACGTTT CCTGTCATC	GGTTGGAACT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTTGTGGCTTGACAGGTTTGGTTTGTGTTAAGTTAGATT TGAATCCTTTAAAGAAGAAAGTGCTCTTACGTTTACTACAGACCTCATCTCCTGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAAACC TGTTGG
WI-2033	183	T C A	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAGGTTATACAGGACCAGTGTGGAAATTTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T C ---		---	TTATGGATACATGTTTCTGTGGGAAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCCTTCCACCATTCTCCATCTACTTTCTACTCTGA[T/C] AGGCAGACTTATATGGAATAAGGGA
WI-2034	150	T C C C A A G G A C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAGAGGCTTTGAGGACCATGTGGGCCCAAGA CCTCCTTCTGCGGTTTCAAGTGAAGACGATGAATCCTTCACTCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTATCTTTTACCCCTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TG T G C T T T A A A A G T G T G T A A G T A T T A A T T A G	A T T T C C T C T T G A A G A A A C A T C A	T C A G G T G A C A A G A A A A G T C A C A T T T C T T C A A T C A C T C A C C A T T G T C T G T T A T T G T C T C T T G C A G T G T A T C C A A G G A T G T C A C T T T T G G A A C T C T G T A G A T C A G A A A A A C T G T C T T T A A A G T G T A A G T A T T A A T T A G A T T C T A T T T T G A T A C [C / T] G A T G T T T C T T C A A G A G G A A A T T T G T G T A A G A G G A T T C C C A T T T G C A T T C C A T T G G C
WI-4782	113	C T	G A T G C A G A A G A T A A C T A G A A A A T G C	G A A C T C T T C T G G T T A T T T T T C T G T T C	T C A T T G A C T T T T A G A G T T C C T C A G T C T T T A T G T C T T A T T C T T A G G A A A A A C T A G G C T A G G A G A A C A C A A T T C A G G T T C T C C A G A T G C A G A G A T A A C T A G A A A T G C [C / T] G A A C A G A A A A A A T A A C C A G A A G A G T T C A T T A T G G T T T T T T C C A G A A C G A T T A C
WI-4788	65	A G T T C C	G C A T A G A A T C A T C T T G C T A A G A T T C C	G G A T A A A A T T A A A A T T T T G G C A T A A	A G G A G A G T T T T G G C T C T T T C C G G A C T C T T G G A A T T C A G T G C A T A G A A T C A T C T T G C T A A G T T C C [A / G] J T G A A A A A A A A T A T G C C A A A A T T T A A T T T A T C C A A A C T T T A A G T C G A G A T T A T A A T T G A T A T T T A A A A A C T A T A T T G A G T C T T T C T A A A A G A T G G C G T A C A C T A
WI-5300	38	T C	T C C A G A G A C C A C T T C A T T C	A T T T C A T A A T C C A A A A	C T T A C T T C C A A A G T G T T T T C C A G A G A C A C T T C A T T C [C / T] T T T T G G A T T A T G A A A T A G A A A G A G T A G G T G T T A T T A T T C T C T T T T A C C A A G G T G A A A T T G A G G C T C A G A G A C A A G G T A G A T G A T G A G C C C A A G G T C A G T G A C A G A G C C A
WI-4818b	121	G T	T G A T A A T G G G G C C C T G T T	T A T G T A T G C C A G A	T A T A A T G T T T T T G T T C C A T A G T T G C C A T A G A C T A G G T T A T G T C C A C A C A T G A A T A A A C A A T C T T A T A A T A A T T A T T C A A G A A G A A A A T A T A C A T A T G G G T G A T A A T G G G C C C T G T [G / T] C T C T G G C A T A C A T A T A A A G G A A G G C T A A
WI-4818a	43	A G C	T T G C C A T A G A C T A G G T T A T G T C A G C	C A T A T G T A T A T T T C C T T C T T G A A T A A A T T	T A T A A T G T T T T T G T T C C A T A G T T G C C A T A G A C T A G G T T A T G T C C [A / G] C A C A T G A A T A A A C A A T C T T A T A T A A T A A T T A T T C A A G A A G G A A A A T A T A C A T A T G G G T G A T A A T G G G C C C T G T T G C T C T G G C A T A C A T A T A A A G G A A G G C T A A
WI-5317	139	T C	T T C C A T T T C T G G T A G C A G G T	A G A A A T G A G T C C	T T T T C C A T T T T T G T T G A T T C T T T T G T C T G A G C C C T T A G A T C T C C T T T A A A T T A A T A G C A A G G T T A A T A A T A T A A T A A T A T G A T G T T A T A T A T T A C A A T T C A A C T C A A C A G G A A T T C C A T T T C T G T A G C A G G T A T A [C / G] G A C T C A T T T C T T T G C A T C T A T T T C T A G G T A T T T G C A G C C C G A G A T C T A C C C A G G
WI-4888	56	G A A A G A T A A C A	G C A A G A T A T A A A G A T T A A G A A A A G A T A A C A	C A A T T C C A C T A C C T C A T T T A T T C A	A A A T G A G T A A C C C A A G T T A C T C G G C A A G A T A T A A A G A T T A A G A A A A A G A T A A C A A G A [G / A] A T G A A T A A A T G A G G T A G T G G A A T T G C T T G A T A A C T G G A G T A G T G C C T T
WI-5328	44	A G	---	---	A A C A T T T T T A A C C A T G C T A C A T T T A C A A C A C T G A A A A G A C A G [A / G] A A A A A A A A A T A T T T T G C C T C A A A A A G C T C T T A A G A G A T T A T G T A A T A A A A A A A A A A T A T G A A T C A G A A A A A G G A A A A A A T A G A A C A C G T G A T A C T G G A A G G A G
WI-4897	93	A G	---	---	G C C T T T T G A G T T T A A G T C T T T T G A G T G T C T T T T T T T T C C C C A C T A G G T A C T C T G G C C C A A T C C C C A A A A G A A A A T A A G C G T T G G [A / G] A T A A A C A C A T C T T C
WI-5345	29	G A	---	---	C C C T G C T A T A G G T C A G T T T A A A A A T C C [G / A] C C T G C T A T G T T T G C T T G T T G A A G C C A C A T C C A C T G A G G T A T A T T C T G T C A T T T C T A T A T A C A C T C A G C T T C A G A T C C A C T C C A C T C C A C T G C A G

TIGR- A004W22	232 C A	GGATAAATCAGTACAATAATGGGACCTTAAACTGCTGTGTGATGCAGGAGTGGGGCTGGCAGTG CCCGAGGAGGGGAGGACAGTGGGACAAAGGATGCTAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCGATGGGAATGACCAGGTCCACATCATGCACGAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTGTGCCCCCGGCTA/C/A/CTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT/AAACCCCAATTT CTC/TTTCAACATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACTTTAATAAATTAAGGAACAAT
TIGR- A005D24 a	123 A G	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATAATCTCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAAT/AAACCCCAATTT TTTCTCTTCAACATTTAGTTGATTATCATCTGGATTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACTTTAATAAATTAAGGAACAAT
U03735	74 C G	TGAGTCTGAGCAGAGTGCAGCCAGGGCCAGTGGGAGGGGCTGGCCAGTGCACCTTCGGGGGC GCATCC/C/GTTAGTTCCACTGCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATTTCTAGTAGTGGTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAAAATGTTCTTTAA
U39840b	42 T C	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAAT/C/CAACAGCAAAACCAACACA CAACCAAAACCGTCAACAGCATATAAAATCCAACAACATTTTATTTTATTTTTCATTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCCAACCAATTTTTTCC
U39840	56 A C	GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAATCAACAGCAAAACCAACACA CAACCAAAACCGTCAACAGCATATAAAATCCAACAACATTTTATTTTATTTTTCATTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCCAACCAATTTTTTCC
WI-8997	41 G A CCCC	...	GTGGCCATCGATCTGACCGTCCCTGCCACTTGCTCCCG/G/ATGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACAGAACTGTGTCTCATGGT
WI-7008	180 A G	TATACCCTTCCATTTGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGACCCAGTTTCATGATAGGAGTTTCAGGTTCATATGTTGACTGATGACCCAGAGTCAACATTCAG TTTCCACCAAGCCCCAGTACAGGCCCAAGAGCTGTCTCTCAAAAG/AGAGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTCACT
WI-9005	26 C T	...	GGTCCCACGAATTTGCTGGGGAATCT/C/G/TTTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGACGGTCTCTCTGTTTCTGGGTTG

WI-7593	46 G A	TTTGTGCTCTGGACACCCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTGGACACTCTCTGAAATATAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCCAA
WI-6962	78 A G	AGTGCATCTTTGGGAAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGA[G/G]GACAAAGCTCCTCAGTGAGCTGGTGATATAATCCAGACAGAACCCCAAGTCTCCGACTCTGGCCTTCTATGCCCTCTATCCTATCATAGATAAGATTCTCCACAGCCTCACTTCATTCACACTATTCTCTGAAAATATCCCTGAGAGAGAACAGAGATTAGATAAGA
WI-7059	43 C G G C C A T C	AAGGCACCCA GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCATC[G/G]TGACCCAGCGAGGAGCCAACTATCCCAAATATACCTGGGTGAATATACCAAATCTGCACTCTCCAGAGGAAAAATAAGAAATAAAGATGTTGTGCAACTCTTAAAAAA
WI-9083	53 A C T T	CACTTCACTGA AAGACACCAT	AGCAGCCATCACATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTAT[G/C]TACCCAAAGGCAGAAAGTAGAACCTACTATTCAATTAATGTTTGACACAATTGGAATTGTC
WI-7079	293 T G	AAGGGCATTGAGACTATAAGCAGTAGACAATCCCCACATACCATCTGTAGAGTTGGAACTGCATTCTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTTCTTATTTCTTTCCATTGCTTATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGTGACTTTCCAAAGCCCCTTTACAGCTCTGGCACTTTCTCGCTAGGCCTGTGAGGTAACCTGGAT
WI-9074	38 A G AAAAG	GATAAGTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAAGTTCTTTTGTCTATAAAGAA[G/A]AAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTATAATTTTAAAGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGCTTGACCCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGTTCTTCTTGGACTGAGAGAAGGAGGCCCCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGCAACAGGTGGGGGCCACAGCACAGCAGCATCTTTG[C/T]
WI-7104	157 C A	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTTCTGGTTGCTTGACCCAGTCACGTTGGGAAGAGAGAGAGTGCCAGGAGACCTGAGGCGAGCCGTTCTTCTTGGACTGAGAGAAGGAGGCCCCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCTGTGTGAGGCCCTTGCAACAGGTGGGGGCCACAGCACAGCAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC
WI-9161	61 C T C C T G G C	GCTTACAGGAG AGACTAGACA GGAA	TGGAGTTTCATGCAAGGGCAAAAGGAGTGCCATGCCAAGCTGTTAA
WI-9014c	93 T C	CTGTGAGGGTGACGTTAGCATTTACCCCAACCTCATTTTAGTTCCTTAAGCATTGCCTGGC[C/T]TTCCTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
			CCCTGTTCCCATGCTGACCTGTGTTTCTCCCAAGTCACTTTCTCTGTTCCAGAGAGGTGGGGCTGGAT
			GTCTCCATCTCTGTCTCAACTTAT[C/G]GTGCACTGAGCTGCAACTTCT

WI-9014b	44 C T	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCGAGTCATCTTC/C/TGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTCTCAACTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAGAGCCCTGGTGCT CAGTGCCCTTAAAGTGCATCCCGCTGTGCTGACTTGTGAGTGGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTGTGACAGAG/C/C/CCTGGCT GCTCAGTGCCCTTAAAGTGCATCCCGCTGTGCTGACTTGTGAGTGGGATCAACATCTGTCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTGTGGACACCTACTAGCTTCCCTTCCCATTCAC CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTGGCCCTCCCT/C/TGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGAAGCAGAGAGAAAGCTGGAGGAAGCCGTGGGCCAAT GGGAGAGCTCTGTATTATTATTATTGTGGCGCTGTGTGTGTGTTA
WI-9171	62 G A	ACATATCTGAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA/G/A/ TTCTTTACAACCGATGGTAATTAAGCTTGTATTACAAAGACTTCATGC
WI-9174	47 T C T	CTAGGACCCC ATTCTCCTATT ACTG	TCTAGAGGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/C/CAGTCTCTGCTCTATATA CCCTCTAGAAACAGAGAAAGCAATTTTAGGACGCTATGGTCAAAATTGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA	CAGAGGTCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAGAACAGATAGATCCCTGTATT TCAAGACCTCTGTGCACCTATTATGAACCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCCTGCTAAGTTAATGTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA/G/A/ACCTAGGTCAGACTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGAATATTGT CTGCCCTTAAAG	GGTGTGTGTGG TAGGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTAGCAATTGACAGAGAATAA CTCAGAAATATTGCTGCCTTAAAGCA/G/A/TACCCCTCCACACACACCCCTGTCCCTC
WI-9015	48 C T	TTGGATTGATATCGTGAATCCTCAGCCGAGAGAAATGGGCTGGATTG/C/TGCTTTGGTTAATACAT CTTCCCTAAAGAAGATAACACAAAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGGA	GGAGCCAGGAGACAGAGGTCTGAGAGAGGCCAC/G/GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGAGCCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG

WI-9231	32 G	CAGTCCCCCA GATTGA	CAC TTGCCAC ACTCAGAC	GTGACCCCTGTGAGGTCCGCCAGATTGAGCTGTGAGTGGCAAGTGTGTCAAAAGGGGC TGCCCCCAGGAGATGAGGCTGAGAGCAGGGAGTTGAGGCCGAAGTCA
WI-7836	120 T C	CAAATAAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGATTGAGATAAACACTCTCATTAGTAGTTACTGAAAGAAAACTCTGCTA GAATGATAAATGTATGTTGTTGTTTAACTCCAAATAAACAAATGCAACGTTCCCTTCGATTCTTAAT CTTGGTTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCATACCCAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCTTTTGGCCCTGCAGCATGTCTGCTCCAGAAATTCAGCTTCAGCTTAACGTGACAGATTC GTTAAAGCTTTCTGGTTAGATTGTTTTCACCTTGGTGATCATGCTTTCCATGTACCTGTATATAT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTT T	CCCAATTTTA TTAAAGTTTA CATCTAT	CAAACTCTTGGAAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTAGTGAAATTTTAAATTCGTTATAGATGTAACCTTTTAAATAAAATTTGGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA TTC	GC TTGAGTGA AGTCTCCAGA	GAAGATTAGGGAGGGTGTCTCTGTGGTCTCTCCCTGCCCTCTCCCA/C/A/GTGGGAGAGACC TGATGTTGCCAAGTCCCTGGACCTGGACCACTACTGGGCTTATGGTTGGGGTGGTAGGCAGG TGAGCGTAAGTGGGAGGAAATGGTAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGACCAG ACCTAGGTGCTCTCTAGGAGGAAACAGGGAGACCTGGGCTCTGTGGAT
WI-9064	29 A G	CGTACCTCCAA ACATAATTGA TTC	GC TTGAGTGA AGTCTCCAGA	CAAGGGTACCTCCAAACATAATTGATTG/A/GTTATCTCGAGACTTACACTCAAGCAATCCTGAGG AATACTGAGGAGGGCTGGCTACTGTCTCTGCACTCTGCTGTTG
WI-7307	128 G T	CGTACCTCCAA ACATAATTGA TTC	GC TTGAGTGA AGTCTCCAGA	CACACTTGTCTGTTCTCAGTCTGAGGTCTCTGGCAGGGTCAAGCTGGGGTAAAGCCGGGTTCCACA GGCCCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCCTGAAGCCAGCTTGCACCTCCAGT TTGCACAGGGATTGTCTGGGGGTGAGGGCCTGTCCCAACCCCGCC
WI-9274	25 C T G	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACCTTTGGTG/C/TJCAATGGACAGAAAAATCTACCTGTCTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTCGAGGTGGAAA
WI-7313e	266 T C	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTTCAGCTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATCCCTATCATATCTTTATT AATTCAGCCAGTGTATCCACCACTTTTGTGTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C T	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	AATTCCTTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAAT TGTTTTCAGCTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATCCCTATCATATCTTTATT AATTCAGCCAGTGTATCCACCACTTTTGTGTTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTGTAACTGAATAGAAATGTATAGCGATGA

WI-9281	68 G A	GCTAACACITTT TAAAACCGT CTC	---	CATTTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTACAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/ATGTTAGTTTGCAGTCTGTGTGCTCCCTCTCTTAAGCTGTGTCCC TTCTGAAAATATAACCCAGCCATTGAGCTATTTAAAACTTGTAATTTTTTAATTTACAAAAATATAA AATATGAAGACATAAAACCCAGTTGCCATCTGCGTGACAATAAAACATTAATGCTAACACTTTTTTAAA ACCGTCTC/A/GTGTGTAATAGCTTTCAAAATAAATGTGAAATGGT
WI-7848	142 A G	GTATATTACA ATGATCACCG ACTGA	CCCACAGAAC TATTGTAAAC AA	---	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATTGCTTTGTATTGTATATTACAATGATCACCGACT GA/G/A/AAATATTGTTTACAATAGTCTGTGGGGCTGTTTTTTTGT
WI-9304	70 G A				TTACAGAAACTTGCCCTGTGCCGTGTGCCCTGTCCCCCATGCTAGGGGGGAGGGGTCTTTTCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCGCCTCGTATCCTACCTTTCTCTTGTCCCTGGCTGGCTGCAC AGAGGATTGCCCCCTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATTGGCTGCCCTGGTGGGAGGAACCATAGTCCCT
WI-7933b	314 C A		---	---	TTACAGAAACTTGCCCTGTGCCGTGTGCCCTGTCCCCCATGCTAGGGGGGAGGGGTCTTTTCCTCTCTTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCGCCTCGTATCCTACCTTTCTCTTGTCCCTGGCTGGCTGCAC CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCAC CAAAGTCTAAGGGACCATTGGCTGCCCTGGTGGGAGGAACCATAGCT
WI-7933	96 G C		---	---	CCCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTGTAAATATTTTGAATGTAAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTGAAGAATATATTGTT/AJ/CAGAAACACAAGGCTT GAT
WI-7374	182 T A		---	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTCCCTTCTCCTCTGCTTCTCCTCATCATCATTCCTCCCAACAACAT CCTCTGCCA/C/TJACACAACAAACGTAAAGTTTCATTTGGGCAAA
WI-9343	78 C T	CCAACAACAT CCTCTGCCA	TG		CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGCTGGGATGATCTCCAAGTCTGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAAATTGTTA/TJ/AJGTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-7386b	104 T A		---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTTTGTATTAT GCTCTT/A/GT/GATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9357	75 A G		---	CTTAGAAAA TCTGCTTTAAC	TGAAGGGGTGTGGCATCTGTGTTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTGTG CTTTAACTTGGT/CJA/TTCCTCTAAATTGTTTCCCTAGGAAATGACTGTCCCAAG
WI-9360	79 T C	CTTAGAAAA TCTGCTTTAAC TTGG	A	CCTAGGGAACA CAATTAGAGGA	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCTTTTGAGGAGTGGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTCCTGGGCTGTTCCT/CJ/CJGGGCTCTCTCGACCTTGCACCGTG GATACAGGCCCATGTGCCATGTGTTTGGGCTCTGGGAGGGTGGGTGAAATAAAGGCATACGTCTCT
WI-7423	107 T C	TGCTGGGCTGT GCTTC	GGTCCAGAAGA GCCC	GGTCCAGAAGA GCCC	

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAGGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTTCATTCGTCATCCAAAGAGAGAGAGGAAAGAAAA [T/A]ACAACTTTCATTCCTTCTTGACAGTTTCATAAACATTCATATA
X86400	118 A C	---	---	TCCTGCAAGAAGTTCTCAAGCCTTTTTGATTTTTGTGCAATAAAGTACAGCTTTCGATAAGAGTGAAA TTGGCTAGCTTAAATGGATCCATAAACTTCTCTAAATTTAAGTGAGA[A/C]TCTTTTAAACACCT GTTAAATTAATGTAGCAGTCTGAGAATCTAAAATATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
WI-8053	242 T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTGTCCACAGCAGCAGTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAGAGTGTCCTTAAAGGGGACTTTTATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAAGGGTCACA ATTAATCTTTGATCTTTTTTACTCACTGTTAACTTATATA[A/T]TCAGAAC
WI-8190	165 G A	---	---	TACACAATGAATTGCTTTTATTCGGTATGCATCCACATTCAGCATTTAGTGTCTCTGAACAGCAAG TGGAAAGACGCGAGCAATTCGCCAGGAGGTCAAGCCACCAATTCGGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG[A/G]AAGCAGCAGCAGCACCACCAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
WI-8275	148 G C	---	---	AACAGTACCACCAACCATATGACAACTGCCAGGCAAGCCTTCTCCCTCCCTTTCGGTCCC ATGTGCTAGTCAGCAAGGTGGGGAGGCCACCGATGTTAGCTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAA[A/G]GGAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAAC[TGGTATGCTGAA
WI-8421	41 G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTTATTGTTG[T/GGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGAGCGGAACCGTACCTGAGAGGGATGGGGCTCTCTCACAAA GAATATTTGGGCGAGAACCTCTGAACTGGCCACGAGGACATCCCAAATATCCCTCTCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-8905	215 T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACAGCGTCAAGCGTCTGGGTGGCAGGGCCATGCTC CTGTGGTCGGGCTGCTCTACAAGGGCTTCACTTTCTTCCACACACTATGTACAGTCACTGCTCCAA GGTATGGGCTACAGTGTGCTGATCAGTGTGCTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAA[T/A]AGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAAAA
WI-9420	202 G A	---	---	AACCTGTTTACAAAAAGGCTTTGCAAACTTCATTACTGAATTTGAAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATGGATAATGATCATTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACGACAAAGGTGCAAGGAAACCCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCACTTCTCACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A	TGGGGCTGCTTTTAGACTTCATTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTGGCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTTAAGAAAAATGGGCTTGTTTCCAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A	ATGTCAGAAGAGACACAGCAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCCAGATTCTACTAGACCGCTGGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	TTCAAGTATAAGGACAGGCTAGAACAAAGGTTCCCAACCCCTGGCACCATGACAGTTTGACCCAAA TAACCTCTTGTTCAGGGGACTGTCTACACATTTGTTGGGATTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAATGAAAAATGCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAAACATATGTTTCTTGGCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCCCAACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAAATTTTCCAGTAGTTACCAGGCACCCAGCCTAT TGGAAGAAATCATAAATGTAAACCTACAATGTATTGCTCTGCTGCTTGGTGGCAGGCATAGAGTT/G JGGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A	TGGTATTTTTCCTTTTCTAAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACACAGAAAGAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGGAATGAGAAAAGCACACCAACGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTTCCTTTCTCTAAATGTTATGATTAAATAGTGTCTTTGTJAGJGAAATTTGAAAAATGT AAATCAGAGAACAGAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGAGAGGGAATGAGAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5896	61 C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTAGTGTGCTGATGAGCCTTAGTTTCJCAJTA AAGCCCCCTCACACCGAGGACAATGTTCAGAACTAAATGACTGAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGGTTATTTTAACTT
WI-7461	153 C T ---	---	TATTACTAGTTTCATAGAGCCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTTCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGAGCTGTGCTTCJTGTTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAAGTCTGAGGCTTTAATGGTCCCTTGTCTCTAAC GCTTTTGGTACTTCTCTTCTGAAGACCAACCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTGACTTCTCTACATTCGTGAAACTAGATGATGAGTCTCTTCTATCT CAATTGAAAATTCCTAGAAJGJAJAAACACCTAATTTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTGTGAAGCCACACAGAGTGTACTCTCTTACJCTJAAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTTCT TTGTCAGGAGTTCTTATTTGGCTTCTTCTAAACCTTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACTCGTTGGCTCAAAGGAAACTGTAGJAJAAATTTCTTTTTTTTATTTTGTGTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAAATACJAGAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGTCTGCTGATGAGGGCATGTGAGCCAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTGTCTGGTGTGCTTGGCCAGTCCCATAGTAGGTGTTCCATAAATAAC AGTGACTAACTGAGGTAGATCAGACAGAGAAATTTCA
WI-11152	179 C T ---	---	GATCTTTGGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAAGTTAAAGGTCTGACACAGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCAJCTCTGTGCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGTTGAGGAGCTGTAAAGCTGAAGAATAGTCTCTGCTCTGCTCTTCTGTTGGAATGGATGAGTCCT TTTACAAAATTTTCTCTCTTCCATGGGTGTTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACTTGAGCAAGTGCTCTTAATGTCTCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCAATTAACAGCCTCCCACTGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAACACACATTAACCTCCTCCCCACTCTA CCCGCCAAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTCCAAACCATGTGTGTTTCTTCACATACCTTTACGTAATTTAAATCATGTCAATTAATTA TGCACCTACTTGTGGCTACAGACATGCTTCCAAATGTAAATCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCTCTAAA[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTTCACCTCTCTGTTTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACTTCATTTGACATCTAAGAAGATAAAGAAAAACACGATCCACTGTGTGTTGCTT GATTT[A/G]GGAGATAAAACCTGATCTTAAGAAAAATTAACCAAGCAGTACACTAAATAGCCT TTGTGTGTTTTCAGGAAAGAAAGCCAACTCAACTAAGTTGCTAAGAAAAATATGTTTCATATCA CTCTAACTTCCACATAGAGCATTATATAGCA
WI-9705	111 C A ---	---	TGAAAGGACCAGTTCGAATGCTTACCAAGGTAAAGTAAATCGAGGGGCGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAAATTCAGGTTCTTAAGGAGTTCCGCTGCC[C/A]AAAAATGTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATTGTTGCTGTGTTCTTGGTG
TIGR- A004Z48	177 A G ---	---	CAAAATACTCTGCTTAGAAGTTGCTCTAGGGCCCATGGATTTCATGAAGGGTGGGCGAGGGTGGACTG AAGATCTGTTGGCAGGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA/[G]TCCTCCAATTTTCAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34 T G ---	---	GGGATTCAATGTGTCTGTCTCATCCAATAAGCACTT[G/C]ATGACCTCAGCCCCATACTCTTTCTCCC TATGTTCCAGAGACAGAAATAGACCTGGCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCCTTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATT[G/AA]AGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTCCTGTTGTTTGGTATCTCTGCCAGTGTTGTTGTAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAAATAAAGTATATAATTTTTTATGTTTGTTCIGA

WI-7747a	44	T C	---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTCGTTAACTGTGATGTAC ATATATATATTTTTAAATTTGATTAAAGCTGATTACTGTCAATAACAGCTTCATGCCCTTTGTAAGTT ATTCTGTTTGTGTTGGGTATCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACCTGTA GTTTACCAITTGTAATAAAGTATATAATTTTTTATGTTTGTCTCTGA
WI-7189	197	T C	---	---	TCCAGAAATTTCCCTTCAGCTCATTTTGCTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCAATATTTCCCTTCAAACAAATAATATTTTACAGAAGCAGGAGCAAAATATATGCGCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTATTTTTATATAAGCCTACAACATTTTTT[C]CJ TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAAACCTTGGTTATT
WI-7850	57	G A	---	---	AGCCCCAGCTGGACTCATGGATGTGCACCTTTGCTCCCTGCTCTTTCTGCCCTCTGG[G]A]CTCATGTA TCTGCCAGCTCTGTACCTCTGTGGGTGCCATCTCTACCTCTGACACAGACTGCCCTGCCCTGAAGCT GAGAAGCAGAGGCAAGGAGCAGGACCAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C	---	---	CTCTCTCTCATCCCATCACCCCTAAATAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[G]C]JAGAAGTGAAGGAAGATAGGAAGGATATTACCTCTCTGTTATTTTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCCTAAATTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATATTGTCAAAAGTTTAAAT
WI-7919	242	T C	---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCCTTGGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGCCCTGGCACTCACCTCTATTCTGTATGATGATGATTGGTTAAACACTGTCAAATAATAGAGAT GTGCCAGATTAGATTTTCTACCTAATCTGTTAATATTGTAACCTTTATTCATTTGAAAGTGTC AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT[C]JACAACCTT
WI-7928	101	T G	---	---	CTCCCTCTCTATGTCTCTCAGCAGCAGTTGGGCGACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTGCACTGCAGACATCGTCAAAATTCAT[C]JACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTTCGACTTTAAAACCTTCAAACTTCAACTCTTATATAGGATTTCTTTT CTATCTCCATCTCCTCAITTAATAAATAACGTACATTTGAGGTAATGGTA
WI-7936	131	T A	---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCAATGAATTTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAACT[A] ACTGAATGAAGAAGTATTTGGTAACCGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAAACAAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C	---	---	TACACGTTCCAGCCCGTTGCCCACTCATCTCGCGCTTTGCTTTGGTTGGGGGCAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[C]JAGCCCAAAGTACAGCCTGGACCAACCCCTGGGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATTGGTGAGATTGGCATGCCATTGAAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G	TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTTTAAATATTTTCATACTCTTGGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T	GGCCAGGAGATTAGCAACAAGGATTCATCTGTTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTTGCGAGTGT [G/T]CTACTCTCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAATTTGGCAATGTCATCAG
WI-140	252 C T	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAAATAGATTTCAATGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTGAGCCAGCTCATTGGCAGAAAAATTCAGGTGAGTGAGTTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTTAAAAATGTGCAATTTGCTGTATTGGCATTCTC/C/
WI-198	218 C T	GAGGTCTTTGAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTGCCATGGTTTGTAGTACCTGGACCAAGTAGTCATTCCATCTGACITTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC/C/TGTTTAAACAAGCATAGATAATCTGAACAACT
WI-205c	146 T C	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT/C/CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-205b	146 T C	TTATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTGT/C/CCAAAGGCTTGATGGGAAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTATTTTGTAGTTCCC
WI-234	165 G C	GAAAGACTGAGTTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCCCT CTCCCCCACAACACAAAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTTCTAGGTGGGCTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G	AGCTTTTGAATCCAAAAACCAAT[G/C]CTGACTCTCTTATCCTCCTCTTGTTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTGTCTATCCCTGATGACTGGGCAAA

WI-276	25 A G ...			AGCTTTGAAATCCAAAACCCACAT/G/GCTTGACTCTCTTATCCTCCTCTGTTGTAACTATCTATCC CTGAGGAGAAATACAGAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTATCTCCTCTGCTATCCTGATGAGCTGGGCAAA
WI-427	59 G A ...			TTTCCCAATCCACAGGTAAACTAATAATGGATGATAGAAATTTAGAAGTACTTCC[G/A]GTTT TTCCCTGGGAAATATTCACAAAACATTTGGTCTGCAATCAGGTAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGGCGTGAAGTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATAGAGCCAGGTCTTGTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ...			CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCCATAATACTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATAACTTCTCCACTTCC
WI-562b	106 T C ...			CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCCATAATACTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATAACTTCTCCACTTCC
WI-562	103 T C ...			CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAAAGCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCCATAATACTCTCAGGTAATTTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACAATAACTTCTCCACTTCC
WI-597c	141 A G ...			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/A/GTAAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAACTAATAACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ...			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/A/GTAAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAACTAATAACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ...			GTGTAATTTGGTGGCTTTGCAACTTTCCACAGTAACCTTTAGAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GAT/GCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTAAAC TTGATCTAATATTCTTCACAACTAATAACCTGAGAGAAATAAGTCTATTAAAT

WI-811	66 G C	TTCAAAATTAACACCATGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGCTCTTGACGTATTACGTATTCGATCAGTCACCCCATCTGGA ACCAAGTTTCAATTTCTGTGACCCCTCCCTCCTCACCCTACTTGGGCTCTGACTTCTTCTCTGGGCT GAACCTTCTGTGTGGCTGTCGGCTTCCCTGCTGGCTCCCAATAC
WI-881b	156 A G	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCAGCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAATCTGTCTGTTT
WI-881	156 A G	TGAAGCCCTCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCAGCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJAGJTATACATATGGCACCATTGGGACACAGATTATATGTCAGA CACCACGNATGTCCTTAAGATATGCAGCAAGCACAATCTGTCTGTTT
WI-867b	119 G A	AATCTTAACAGCCTTTTGTATGCCAAAGCCACCTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-867	113 A G	AATCTTAACAGCCTTTTGTATGCCAAAGCCACCTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-867	119 G A	AATCTTAACAGCCTTTTGTATGCCAAAGCCACCTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCAAGTATCTGGCAGATCTTCCCTTTTCATCTCCGJAJTTTGTGTTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCACAATAGAAAACCTTA
WI-871b	123 C G	TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCACCTACCTCATGIC/GJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTTTGTACATAA
WI-871	123 C G	TCATCAGACCTGAGATTGAGATGAAATCTACCAAGGTACCACAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCACCTACCTCATGIC/GJAACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGCTGTTTGTACATAA

WI-884	198 TC ...	---	AGGTTCTGGACTGATGCTGGGAAACAATTGGGTTCTGGAGAAATTCCTATTTTGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTCCTGATCTATTGGGA ACTTCCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCCGCATGCAACATTATTTCAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205 GA ...	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCAGCCCTGCCGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205 GA ...	---	CACCTCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCCTCAGCCCTGCCGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90 GC ...	---	GGCTGGGATGAGAGGTTCTACTTGTTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 GC ...	---	GGCTGGGATGAGAGGTTCTACTTGTTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGCCCCCAAGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCATGACCAAAACAAAGTTCAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 CT ...	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTC[T/C]TTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 GA ...	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTTCATTGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 TC ...	---	TCCCACTGAGTATGGCTTTTCAGTAGTTTTATTATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTACTTTGGGAGAAATGCTCAACTATAAATATGCTTCTGACCCCTTTCTGTTCTG CTTCTTAAAGATACAAAATAAATGTAAACATTAGACCTCTCAGTAT[C/G]GCTGTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTTATTGCTCTGGCTTCATTTGTAAATNG

WI-1147b	204	G A	---		TTTGGCATTATTTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCATTACCATAAATCACCTTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C T	---		GCATTGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGATGGTCTCCTGAGTGTCTGAAATG/C/GGCCAGGT TAAGTGTGGGG/C/TTCTGGGGTCAAGCTGGCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G	---		GCATTGAGGGTTCGTTTAAATGACATTCACCTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAATGATGGTCTCCTGAGTGTCTGAAATG/C/GGCCAGGT GGCTAAGTGTGGGGTCTGGGGTCAAGCTGGCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C	---		AAGTTACAGAAAAAATACCAAGAAAGTGAATCAAGANTCAGCTGAGATAGAAACATATGCCCCA TCATCTTCAANGTCCACAGACACTTATCCCCTAGACAGCCATTTCTTTTGAATGNT/C/GGNCANT AAAAATGATTTGAAATGGGAATAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCTTAG GGC
WI-1305d	202	C T	---		TTCTCAATCCAAATCTGTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T	---		TTCTCAATCCAAATCTGTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C	---		TTCTCAATCCAAATCTGTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T	---		TTCTCAATCCAAATCTGTGTGTACTTTTATTTCTTTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTTGTGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTA/GJGC
WI-1306	240 A G	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTTGTGNNNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAAATCTGAAGCTGTGACCTAAGGNGAGAAGTGCCCTNNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GJCTTCCTAGC
WI-1307b	118 T C	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTTGCTGTGTTTCTCTCTGTAAGNTGTT
WI-1307	118 T C	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTCTCTCACTTCTCAAGTGGACA GATTTCTGCATTACTGCTTGGGTTGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGCTTT CCTACCTCTTAATGTATCTTNCATTAATATGCTAAACCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTGTGTTGCTGTGTTTCTCTCTGTAAGNTGTT
WI-1325b	169 T C	GAGAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTCTGTGGTTTTATCGCAGCAAGCN ATGTCGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T	GAGAGATGGCCAAAGACAAAGCAGAGGGGAGAGAGCAACCNCTCTGTGGTTTTATCGCAGCAAGCN ATGTCGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATAGGCAACTACAATGTGCCCTTGTCTCCTT/CJTTACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGCTACCAAGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175 C G	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGCGGTTAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGGAAGTTGGGTAG/CJGTACCAAGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136 GA ---	---	TATCAGCATGATTGGCTGTGGACACAAAGTCAATTTGTACTTTTGTGNNNTCCTTTCTNNTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTGTTNAAATATACCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTTCTGTGCTTGGACACAGAGTCGCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCTCCAGCCACCTTGACCTTAGCAAGTGT
WI-1349e	192 GC ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]JTTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 GC ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGA[G/C]JTTCAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 CA ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTTCAAATA ATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 CT ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTCTCGCTTCTGACCTTTGGTAAGTTG[C/J]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTCA TAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGTCTCGCTTCTGACCTTTGGTAAGTTG[C/J]TCCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCTC ATAATCCCCAAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31	C T	---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/JTTGGCCAGGGCGGCAGATGTAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGGAGGGCCCCAGGAATCCAGTGGCCCTCTCAATGACTTG GGGTCTCGACTTCGGAAGTTTAAGGGCTCGCTTCAAAAAGCTGGTCCGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTTAATGTTTGTCTTTAGAAAAAGTCGC
WI-1417b	31	C T	---			CAGCCGGAAGAGATTACGTGGAGAGATGTC/JTTGGCCAGGGCGGCAGATGTAGCCACGGG GGTGACAGCATGCTGCTGGCAATTTGGAGGGCCCCAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTTAAGGGCTCGCTTCAAAAAGCTGGTCCGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTTAATGTTTGTCTTTAGAAAAAGTCGC
WI-1729	172	A	---			CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCAACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTCTCTCCGTGGTNACTTCTCTCCACCATCACCTGTGTTTT
WI-1732b	122	T C	---			TGCCTTACTTCTTTGTTTCAATCCACCATTTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCTTTT/CJATTCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114	C T	---			TGCCTTACTTCTTTGTTTCAATCCACCATTTACATTTTGTAAATTTGAACTTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGACATATTCAGGAGTNTCCCTGGGTCAACCTTTTACCTTTTATTCAGTCT CTGCCACATGCTAGTAAGTGTGAGTGATGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97	A G	---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAGGTTTAAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGJ/GJTTTAAAGTGTGCTGTTTTCTGGCAAGAGTCAG TGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31	A G	---			GGTACACAAAAGAAATGCTTCTGGAAATCTACJ/GJTAGGCCCTTAACATTTTGGCTGAGTATTAATC TGACATGTGTAATGTGAACCCACCATGAAGCTGGGCAAAAGAACAAATTCCTAGGAAAAGTACAATTAC TGGGAACTGTAGAACAATAATTCATAGTTTACACATAGCTGGGAATCACTCATGTTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77	A G	---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGATJAGJTAGGTAGGATGAGCATCACACTTGGGAGGACATAATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ...			CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATGAGTAGGTAGAGCATCACACTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ...			TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACTCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGOCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACACTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
WI-1837	112 C T ...			TTTACTTGGGATTTTCATAGCTGATCATAATTTACCATTTGATAATTCACTCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/C/TCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACACTGGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
WI-1840b	79 G T ...			TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G/T]GAGAATCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ...			TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G/T]GAGAATCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTTATCTCCAGAGTGTTTGAATTTACTAAAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ...			GGGCTCACTTTTCATCAGAGCACATATCAGGTAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TGTCTGCNAAATAAACTCCCAAAA AAGTGTTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ...			GGGCTCACTTTTCATCAGAGCACATATCAGGTAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TGTCTGCNAAATAAACTCCCAAAA AAGTGTTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ...			TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTTGCCCAACCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTGCATGAGAAACCACTTTCTTTGCTOC

WI-1900	119	C T ---	---	TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATATGAATAATCAACTGGACAAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCATTTACAGCTGCAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACCGGCACAACTAGAGAGCAGCCAAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAACCTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165	C T ---	---	ATCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T ---	---	ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T ---	---	ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGTAGGGAAGACCAGCC[C/T]CTCTGAANCTGGTCCACGCTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAGGTGCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T C ---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTTAGTCTCGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTTT /C/TAAACAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102	T C ---	---	AAATCTAGAAGCCAGAGTCAGCTACGATTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATTCTGCACAAAACCTAGCTAAAAATC/TCTTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACTTTTTTCTACTCTCATTT GGCTTACCAATGCTTCCACTGGATC

WI-2013	127 C T	---	---	CTTTAGAGTGGTCAATTCGGTCCCTTCTGGAAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATCTGACACTC/TCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCAGTGGAGGGATATCTCAGCTTCTGAGCCCTGGTACTGCAATCC
WI-2032c	166 G A	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACAC[G/A/TGTGGACCTCTGTCTCAACCTCCGACTTTCAC AGATCATTTGGTTAGGCTCACCTTCCGTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032b	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/G/CTTCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2032	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAAACC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGACCTCTGTCTCAACCTCCGACTTTCACAGA TCATTGGTTAGGCTCA/C/G/CTTCTGTAATTGCTTCTGTTTTTCAAAGGG
WI-2054b	188 C T	---	---	CGTTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTC/TCTGCTCCCTCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2054	183 T C	---	---	CGTTTTCTTCTACATCTTGGGNACATAAAGANGAAAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTCATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTC/TCTGCTCCCTCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
WI-2573d	129 T C	---	---	TGGGATTAACCCCTGTTTTCTTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTTCCGTGCTTT/CJTGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCCTAGGTAAGGGTAAGCAACACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165 A/C	---	---	TGGGATTAACCCCTGTTTTCTTCTCCAGTTCAGTGGCTTAATGTTTGTGCTAGAAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTACAAAGGTGTTTCCGTGCTTTGATAT CATCTGATCTTCCCAACAGGGCTTATTTA/CJTGCCTAGGTAAGGGTAAGCAACACAGAGGCTGTG TGAAGTGAATGATTTGCTTGCACAAGGTATATGGCTGGGCTTGGACGAG

WI-2573d	129	T C	---			TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573c	165	A C	---			TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJ/GA CATCTGATCTCCCAACCAGGGCTTATTT/CJ/GCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573b	165	A C	---			TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTATATGGCTGGGCTTGGACGAG
WI-2573a	129	T C	---			TGGGATTAAACCCCTGTTTCTCCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCCGTTCAAGGTGTTCCGTGCTTT/CJ/GA TATCATCTGATCTCCCAACCAGGGCTTATTTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTATATGGCTGGGCTTGGACGAG
WI-2868b	60	A G	---			GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAAGCAAGCTTTCCJ/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G	---			GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAAGCAAGCTTTCCJ/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCCAAGTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C	---			CATGCTGTGTAAACCTCTGTGCTGCTGCTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C	---			CATGCTGTGTAAACCTCTGTGCTGCTGCTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGTCCACTTCTGTTCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49	T A	---	---	TTAGCACATATCTGTTGGGACTTAAGTACAGACAAGGCATAAAAAATTAACAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGAAAGACTCTATTCCTGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAAATAAGTCCA GAG
WI-2954b	41	A G	---	---	TTAGCACATATCTGTTGGGACTTAAGTACAGACAAGGCATAAAAAATTCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGAAAGACTCTATTCCTGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAAATAAGTCCA GAG
WI-2954a	38	G T	---	---	TTAGCACATATCTGTTGGGACTTAAGTACAGACAAGGCATAAAAAATTCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGAAAGACTCTATTCCTGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAAATAAGTCCA GAG
WI-2971b	62	T C	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGAATTCJG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGTAACCTCCTCTCCTTTCTTAATAAACCTAAG ATTTCCTTTGTTCCCTGACATCTGGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAAGAAACCTTTTACTTAGGGATTTGTCT
WI-2971	62	T C	---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCCAGTTAGACTCACCAGCATTTCTAAGAATTCJG CTGCCAGCACCAATAAGCTTCTTTCAAAACAATTTGTGTAACCTCCTCTCCTTTCTTAATAAACCTAAG ATTTCCTTTGTTCCCTGACATCTGGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAAGAAACCTTTTACTTAGGGATTTGTCT
WI-2995d	133	A T	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTA ATAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151	G C	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTA AATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133	A T	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGCTGGANTTTTTTTA ATAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNTATCAAGATAAGACCTGGAAGACCCGAGCCAAAGGAAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85 C T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCAC ATCTCAGTTAGTCTCTTC/CJTCCGATATCCTGTTTCCCTTACTCCTATCTCCTGAGACTTCTTCTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACTTTGCAAGG
WI-3234b	68 T C ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATGAGGTCCATGTCCATTACCTCTACTTA T/C/GACAAGCAAGAACACACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTCATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68 T C ---	---	---	ATTCTGTAATGTTTTCACTGCTTCCAGTAAATCTTTATGAGGTCCATGTCCATTACCTCTACTTA T/C/GACAAGCAAGAACACACAGAAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTCATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGGACAAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A	---			GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGTTAATTAATTAAGTAAAAATATTATTTNCCATGA GACAAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
WI-3292	106	G A	---			GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[GA]TGGTATTGGATTGGGATGGATTACTT GCCATGAATATTTCCATTGTTCTCATTAATGTTAATTAATTAAGTAAAAATATTATTTNCCATGA GACAAATGGAAAAATGGAAACATTTCATGGAAAAAACCCATTTCATC
WI-3355	19	G C	---			CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCACCTTAAAACTCATCAGAA AAAAATCATCAAAAGTCGAAGTTAGTTTNAITACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A	---			CCATGAAGAATGAGTTCTCCCTCCCTGGTCAAGTCTAAGAAATAGCACACCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTTATGCTTTNAGCTTT CTGGAATTGGGATGAATCTNACATTCATGTGACCCCTTCGTGTGGATCACTTCTCC[GA]TGGCCC ATCTCGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG
WI-3505b	131	G A	---			TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTCACTAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[GA] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3505	131	G A	---			TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTCACTAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[GA] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTGCATAT
WI-3564b	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[CT]AACAAAGTGTGTTGTGGTGTCTC AGTGTCACACATGCTACCTTCTTCCACAAAAA
WI-3564	177	C T	---			GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTCACATGGCACAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTT[CT]AACAAAGTGTGTTGTGGTGTCTC AGTGTCACACATGCTACCTTCTTCCACAAAAA

WI-3649	64	A	---	---	AATGTCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGAAGATTCAAC[AG] AGACCAGTTTGCCCTTCACTTAGTAGGCCAATGATAGACTTTTAGTGCTACCAAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCGTGGCTTGGTC TTCTGTTTTACCATATTATGATGACATGCAACCTCAGAGCCTTTTA
WI-3674b	133	G	---	---	ACAGTACACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACGAGCGGAGTGCTTTTATAGTAATTTAAATATGTTTATTTAGAAAAAACAACAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3674	133	G	---	---	ACAGTACACATGCCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTCCCTCTCTAA ATTTAACTACGAGCGGAGTGCTTTTATAGTAATTTAAATATGTTTATTTAGAAAAAACAACAAAT[G /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTGGTCAAAATGATTGTT AATCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCACAGCCAAG
WI-3682	137	G	A	---	CAATATAGACCAAAATGACTGCCACAAAGAGAAATAGTGGATCTACATTTAGAAACCACATGTTTT ATTGGCTCTCTCTTCTCTCTCTCTTTTAAATGCTCTCACAACCAATTCAGCTTTATCTTTTCAA T[G/AJAGCAATTTGTCCAAATTTAAAGTCAATGAAAAAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTGCTTATGCTAT
WI-3854b	194	G	A	---	GGTATGTTGAGGTGAGTAAATGGTCACTGGTTGGAGTGAATCTAAATGGAATTTTGGCCCTTGGGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCCTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA GTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G	A	---	GGTATGTTGAGGTGAGTAAATGGTCACTGGTTGGAGTGAATCTAAATGGAATTTTGGCCCTTGGGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCCTTTACAACCTGAGGAAATCAAAGCAAC[G/AJAGAA GTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G	A	---	AGCCAGCCACATCATGTTGAGTCCCTGCTCATCTTCCATCTTATTTCTCTACTGCTTCACTTCACTT CCATTACAAGAACTCTTGATTACATTGATGTTTGTTGGTTACACTACAGAATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATCTATTTGCAATCTTTGTCAATACCATAACATATT CATGG[G/A]TCTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T	C	---	GAAAAATGATGTTTTGATTTCCCTTCCCTATCTTCAGATTATTGGAGTGCTATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACCTGTCTATAATTAACCTTCCCTCTCTGCTTTATTTTGGCTT/CJACA GTTTAGGTAAATAAAAGATGCCCAAGAAATTCAGTATTCAGGTACAGTAAAAAGTAGCAACCATGGG GTAGGGCAAGTNCAGAAAAAGGAGGAGGTGGGGGTTTTCTGGGAAGA

WI-4110	130 T C	GAAAAATGATGTTTTGATTCCCTTCCTATCTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCTCTCCTGCTTTATTTTGCCCT/CJACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGAGGAGGTNGGGGGTTTTCTGGGAAGA
WI-4119b	168 G A	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGGAAGAACAGGACAGAACAGACAGAACGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168 G A	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGTGGGAAAAAGTAATAAATAG AATGGAAGGATAAATAAGGTAACTACGGGGGAAGAACAGGACAGAACAGACAGAACGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51 T G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAAATTTAGTGGGG TTCTTCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 T G	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTCCTCGTTACATAATTTGATAGAAATTTAGTGGGG TTCTTCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTCCATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 G C	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATACT GTGCTG[T/G]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAACGTGAT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137 T C	TTGTACATGTTTCATTCATCCCTCCCATTCCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC[T/C]GTGCTGTGCCCTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAACGTGAT TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188 G A	TAACACACTTTTCAATTTGGTTTCTTACTGAGTTAAAGGACCATCCATTATATACAATTCCTC AGTTCTATGCTTTAGAGTNCATATAGGACTACTGTAAATTTTCAAGAGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAATTCCTAG

WI-4230	93 T ---	---	AGAGACGTTGAATGGGACATCTTTCTATTTTCGATTTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGTACATTCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAATAATAACAGCACACTGACT TTCCATGGTAAAAAGAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGATGACCTTTGAAATTTGAATTTATGG
WI-4241	118 C T ---	---	GAAATCCATTGAAGTTTGAACCTTGAACCTGATCTCATTAACTATTTNCTTGTAGTGGTTGATTT CATTTTGAACAAGAACAGACGAAATTTCCACTTAAATTTAAATCTCIC/TTAAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCTAGATATCTTCAGAACTAGGATGGAAG AA
WI-4271b	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGGAAAGCGGTAA
WI-4389	156 G A ---	---	AATCGAAACATTGATTTTGTAAAGGAACCCACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATGCATAACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGGAAAGCGGTAA
WI-4488	31 A G ---	---	GATGACAATTATTGTGATTGGCATTTTAAAG/G/GTACCATTCATTTCTTCTGGCTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTTAGTCGTATTGCTCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	ACCATCAATGTATCACCTCTAAATTTATTAGATGATTAACTGGCTCTGTAAAAAATAAAAAACCT GTCTTGGACATTGAAATAAAACATTAATTTGTTGCTACTTCTGCTACTTACAAAGGTACTGCACCTA AACAAAGTTAAG/G/C/GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAATTTCTACCACTGTCA TTTCTGTGCCATAAATAAATTTTACATGCCT

WI-4584	144 A G ---	---	---	TTGGTTGGCATTAGCCTCATAACAACATATTACAATCATAATTGTTACTCTTATTTACAAACAAG AAAAATGAGGCTTAACATCAGACTCTGCTTAGTCGAGAGCCAGGATTTGAACCCAGGAATCCATT CACCGGTACIA/GTGTCTACCTGGTAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTTGAAAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185 C T ---	---	---	TTTCTGCAATTTGAATGTGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCAATTTATCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATCCACCAATTTAG TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA/A/- JGATTACTCATAAAAGCATATTAAATTTATAATATGAAAAATTTAACTAGATAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAACGTGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	---	GCCTTTGAGAAATGAAAAAGGGAGCCTGGACCATTCAGGGCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTAT[C/T]GTCTGTCTCCCTTCTGGTATGCTTGTGCATGAAACAAATGAATTC CCCAGTGCTGGCCGATTCGTGGCTCCTAGAGGTGCCAGAAAAAGTTTCGGTGAATAGAATTG ACGAATGGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAAAACGAAT
WI-5404b	87 G A ---	---	---	CCCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCCCTTCAGCAGTTCCATGTCGTGGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACA
WI-5404	87 G A ---	---	---	CCCTTGCCTGCTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTAATTTAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTTGTAGTNAATTTG AATCTTCCCTTCAGCAGTTCCATGTCGTGGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACA
WI-5545b	77 A C ---	---	---	TAGGAAAGGGGATGGTGATGGCTCTGAGACATTTAAATCTATCTTTCCACACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTTCTGACAGCCCAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATGTTAAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCATTCA
WI-5545	77 A C ---	---	---	TAGGAAAGGGGATGGTGATGGCTCTGAGACATTTAAATCTATCTTTCCACACTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTTCTGACAGCCCAAGTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATGTTAAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTCATTCA

WI-5860b	134 A G ---	---	---	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGGCTAAGATTTTATTGT TTCTTTTATATAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GTTTACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	---	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTGGCTAAGATTTTATTGT TTCTTTTATATAAATATGGATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACAC/A GTTTACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	---	GCAACAACCTATTATACCTGATCCCAACCCAGGTCTACTAACATTAATCAACCTAACCAATAC TATATTGCTGTTCTGAATTTATTTCAATTTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATTC/GTATAGTAGGTCACCACAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCT/C AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109c	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATG TGNAAAATTATCCCTGAAATTTTATACCA
WI-6109b	147 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCT/C AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109a	129 T C ---	---	---	AAGATAGACAAACATATGCCAGACCAACAAAAACACAGACCTGTCATATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAAACGAAAGGAAAAAACCT/C AAACCTATATTNCTGTCCTGTCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6112	96 T C ---	---	---	AATGCCTATCACCTCCATCATGCTGCATAACTGATTGATCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTGTTCATGAT/CJGCATATCCCAAGTGCCTTAGACAATGCCTCCCATAC AGTGAACAGTATTGACTAAACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

WI-6244	103 T C	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAGGAAGAGAATAATTCCTTTCTTTTAGTGATT GCTTAATATTAATTATAAAGTGCACCATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAAGCAACCAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTTCCTTCCCAAGGATGGATACATTCTAC
WI-6268	124 C T	CTGGCCTTATAATCCAAGTTAGGATTATCTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGGCACCCTTTGGCTCATTC/TACTCTCCCT GGGTCTATTGACTTTCAGGAGCCTAGAAAGAGCTGGACAAACCTGCTTCTTGCAGAAAGAGTCG GGGTCCAAGATTTCGTTACGATTTTITA
WI-6336b	234 C T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCAATGAAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/CTTJGAGGACACTGACAGT
WI-6336	234 C T	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATAATCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCAATGAAATGGACCATGTG GTACCCAGTGCAATTATGCTTGGTAGAGCC/CTTJGAGGACACTGACAGT
WI-6381	92 C A	TTGGATACAAAATTCAGTTACACAAATCAGTAGCATTCAAATTAAGTTATGAGTATTTATACAATTA CAAAAATGNNTTTCATGTTTAAACAA/C/AJGTAATTTAAAGCTCAAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAAG
WI-6436	198 C G	GGTTGAGGCATTGGGAAGGCAGAAATTTGAGGAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGAGTAGTTGAGTAGGTTAGCGTT/C/ G/ATTGGGTGTATCCACAGACAAGGTGATGTTCTAAGATTGATATTATTGT
WI-6449	186 C T	GAGGCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTCACTGCAATTCCTCTGATCTTATGTCGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTGACAGCTGAAGTTCCTCTAAITTTTCTGTGGTGTATTATA
WI-6449	186 C T	GAGGCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTTCTGATTGGTTGGTGTGCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTCACTGCAATTCCTCTGATCTTATGTCGGCTCTATT/C/ATCCCTATTCTCTGA TCTTATGTGACAGCTGAAGTTCCTCTAAITTTTCTGTGGTGTATTATA

[illegible]

WI-6608b	46 C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTACGGCAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGT[C/- JAGTTACGGCAGCTAAAGGAGGGGATTTCTCTCTAGTCTCTCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTAATTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 C A	GTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAAAGAGGAAACCTCCCC A[C/A]AAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNTTCTCAAGTTCCAGGCTCTTGGGTAGACCAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G	AGATTACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTACGGCCGAGTCAAGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
WI-6670	120 A G	AGATTACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/G]TTGTTAGCCA GCATTGCCATTACGGCCGAGTCAAGGTTGTGGGCCAGAAAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
WI-6704c	33 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C/C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C/C]ACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C	TTTGAAAAATAATTCATGCACCAATGTTTAACT[C/C]AACTACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTTACAAATAAGTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTGTTCTTCCACATGGTTATT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ...				CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACATTTTGTAGGCTGGAATGATTCCTC[G]ATAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTACTATTTACTAGTGCACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ...				AAACAAATGGTGCAATTGCATAATATTGTGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6766	148 G C ...				AAACAAATGGTGCAATTGCATAATATTGTGGTCACAGTATAAAACAATAACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTTAGGNTCTGCACACATATTATCACTGA GAATTTGGTCAACAGTGGAGNGAACTTACCCAAATCCAGTCCCTTCTTC
WI-6787b	97 A G ...				ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTCAC[G]JTCTTACTGCATAAGATATCTTCATGTACAACGT ATGCTTTGTCTTCTGGGAAGGACGCTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ...				GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGTCTTCAAATCAATCAGTCAACCCCTC[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCCGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAGGCAAC
WI-6810b	37 T C ...				CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ...				CACAATAATAAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCATTTTTTAAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTAGTCTGTTACNGCCCAAGGGATAAGGCTGAACAATA AATTAACCCCTTAAAAATGCTATGNACAAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ...				GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTCACTCAACAATGTAGCT GCAGGGTAAAC[C/A]TGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGTTTCAGGTGCGGCCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTGTGTCAATCTTGTTTCAGGTGCGGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACITTTAATGGAAGAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTAAATAGAAGACITTTAATGGAAGAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTTATCCCTTTTAAAACTCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATTTATCCCTTTTAAAACTCCTCTCTCTCTGGTCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAAATATTCACATAAGTAAATACAGCAGATGAGATGCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTAGTCAACTTTGAGTAAATTCACAAATATATAGCAGCTCA AACACAAATGCAGGACACAAATGGCAAAAGTTTGCAACTGTTTGGGCTAATT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGCATACGNGTAAATGAACCTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGTTGTCCTGAAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTGCGAGGCAAACTT[C/G]ATGAGCCATTCTGTGCAGAGAAGGAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATTTTGGCTGTTAGAACTGAGCTCAATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGATGC AGACTTAC[T/A]AGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATAC GGAATAAAATTTCCCTTTTGGCAACAGGATATTTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163 G T	CACTCAAAACCTTTATTCATTGATTACAAACTGTACAATATTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAATAATATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A	GCTGTTTTTTTTGTTTTTAAGTGACACCTTGGCCTTGTTGGCATTTCTTCACTTATCTTACCC AAAGTGCTTTGGCCAGCCACTGACTGATTTAAACCAGAAATGTGTTTTAAACAATGTGGT CGTGGTAATTCAGGTGATTTTCTATTGTTAGTATTTTTCAGATTTCACCAAAAGAACATG TATTGCTTTGTAATTTGAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACTCTGTCCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTCACTGCCCATG CTTTGCTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGTC/CAACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACTCTGTCCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTCACTGCCCATG CTTTGCTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGTC/CAACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCTCAATCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACTATAGGTAGTATTAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79 G A	TTTTATGAACATTTTCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCTCAATCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACTATAGGTAGTATTAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47 C G	AAACTAAACCCCTTATTGTCTCCAAGTGTGGGCAAAATAGAAAATC/GTTTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCAGTCAATAATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTTGAAGAACTGGATTGAAAACCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242 G T	ACTTCTAGTGCCTCTGTTACCAACCCCTCTAATGCCTCTGGTCGCCGACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCGCGGAGTTCCCTG CAGGAGAGAGGGGGCTGCTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGTGGGGCCCTCTGIGCTCTCTCTCTCCG/GTGTGGATC

WI-6996b	242 G T	---	ACTTCTAGTGCCTCTGTTACCAACCTCTAATGCCTCTGGTGGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGAGAGCGGAGTCCCTG CAGGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCCTCTGATGGTGGCCCTCTGCTCTTCTCTTCCG[GT]GTGGATC
WI-6996	228 T G	---	ACTTCTAGTGCCTCTGTTACCAACCTCTAATGCCTCTGGTGGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGACCCAGAGGAGAGCGGAGTCCCTG CAGGAGAGGAGGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCCTCTGATGGTGGCCCTCTG[GT]GCTCTTCTTCCGGTGGATC
WI-7021b	112 G A	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAAGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGTCOCATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGTTCCACATCCACAGCCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGTTA
WI-7021	108 A G	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAAGTTTCTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGTCOCATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCGTTCCACATCCACAGCCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGTTA
WI-7056c	118 C T	---	GGCAGTAGGACCAACAGTGTGGGGTCTGCTGGGACCTTGGAGAGCTGCATCCCAGGATCGGGGTG CCCTGCAGCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA[GT]GGTGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCATTGATA
WI-7056b	118 C T	---	GGCAGTAGGACCAACAGTGTGGGGTCTGCTGGGACCTTGGAGAGCTGCATCCCAGGATCGGGGTG CCCTGCAGCTCCTCCACCTCACTCCATGACAGCGCTAAACGTTGGTGA[GT]GGTGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACACAGAAAGTCATTCCTCTTTTAAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCATTGATA
WI-7091b	153 A C	---	AATTCGCTGAAAAAGGAACTACCTATCCCTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTT[GT]CTTATCATTTATCAGCCCTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTTTATCTGGTTCTATATGAATGCTAT
WI-7091	153 A C	---	AATTCGCTGAAAAAGGAACTACCTATCCCTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTTACTGCTCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATTT[GT]CTTATCATTTATCAGCCCTTTATGATTTTCCAAAGTAAATATTA ACATATTATTCATTGGTCTCTTTTTTATCTGGTTCTATATGAATGCTAT

WI-7136	58 TC ---	---	TGTGAAGCCACATTTTCCAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACCTGT/CJAATTC TCTCAATAACTCAGTGACACTTTAAAGCTGAAGACGACCAACATGAAAGAGCATATCAATGATG GTGGAGAAAGGGAAGGGTTGGCTTTTAAATTTATTTTCTTCATCTTTTATAACAAGAAAGNNNN NNNGTAGCTTTCTATATATG
WI-7146c	210 AG ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATGCC AACGC/AG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210 AG ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATGCC AACGC/AG/GTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202 GA ---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTGTTGGTCACATGGAGCTCTTCCATTTCTGTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGCAGCTGGGCTGTGGATGGAGGGTCCCAACATGGATGTTGGCCCTCTCTCGCATG/AG JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161 AT ---	---	ATATTACAACCTGCTTTTAGCTGATCTTCCATCCTCAAAATGACTCTTTTCTTTATATGTTAAACATA TATAAAATGGCAACTGATAGTCAATTTTGAATTTTATTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAAACNNNNNN/AT/AAAAAAGTTATTTAACAGTAATCTATTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAAATGGTATGTT
WI-7155	156 TG ---	---	TAGAATAGATGCGGTACATTTCTTTGGCTCTGTTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACAGCTGGCCCTACCCCTATAATGATCTGTGCTCAAAATTAATACAC CAGTGGTTCTCTCCCTGT/GT/AAAGACTAATGCTCAGATGTTTACGGATAATTTATATTCTAG TCTCACTCTCTTGTCACCCCTCTCTCTTCCCATTCCTCAACTCCAG
WI-7169b	161 AG ---	---	AGCTCCACAGATGCAGATTTGTTGTTTGTGTTTCTGTTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCAAAGCCATCAAGTGTCTGAAATTCAAATTTGTTTATGCAAAAT ACAGCAAACTTTTATTTAAGTAGAT/AG/GGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCACTTAGCAGCTAGGATCTCAAAATGGAGTGTATATATA
WI-7175b	194 CT ---	---	CTCTAGACTAGTGCCTTTACCTTTTATTAATGAACGTGTACAGGAAGCCCAAGGCAGTGTTCCTCAACCA ATAAATTAGAGAGTCAAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGTTTACTGCTGTCTTGTCCATGTCCTA/C/TJAGAT AAITTTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACIGGG

WI-7175	194 C T ---	---	CTCTAGACTAGTGCCTTTACCTTTAATGAAGTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATAACTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATAATGGTTTACTGCTGCTCATTTGCCATGCCTA/C/TJAGAT AATTTATTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTGGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAAGTGAACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGAA
WI-7178	273 G A ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTGGCTGTCAGTGGCTGGCTCTAGGGGAACAGACCAAGTGAACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACCTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGAA
WI-7182b	116 A C ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCCTCTGCAACCCACTCTGAGCCTA/C/TJCTCTCCTCTATTT TACTTGAAGCTGCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCCTCTGCAACCCACTCTGAGCCTATCTCTCCTCTATTT TACTTGAAGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCAACACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAATGTGTACCTATTAAATTTGTAACCTAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCAATTCCTTAATGTTTTGTTTGGTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTGTCTAA
WI-7199b	112 T C ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCT/C/JGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCAATTCCTTAATGTTTTGTTTGGTGCTGCTGAATTTCTCTTTATTAT AGTCTATAGTTTACTCCTCAGTTCTCACCATCATCTGTCTAA

WI-7216c	237	T C	---			TGACACTAACACTCTAATTAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATTAAGTAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGTATACATAGGAAAAGACACACATCCACCTAAAATGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTTTCTTTGTAATCACTT
WI-7216b	237	T C	---			TGACACTAACACTCTAATTAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTAGATAAATTAAGTAACTTACTCAAGATCCCTCCAGAAAATACGTATGT TTAAAACCCCTTCTCTGTATACATAGGAAAAGACACACATCCACCTAAAATGACTGTACTGTTTAA CTGTCAATTCCTCTGAGGCTAAACACAGTTTGTCTTTTCTTTGTAATCACTT
WI-7220b	147	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCAATTAATTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[AT]AATCTTGAGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7220	140	A T	---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCAATTAATTTGCTCTTTAAGCTGGCAACCCCA TCATTAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA[AT]AATCTTGAGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7226	232	C	---			GATCGAATTTTCAGATGATCGGAAATTTTCATTCAGGTAATTTGTAATAGTGACATATATGTATA TACATACACCTCTATCTCTTAATTTTGTAAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACGATTCCTCACTTCTGGGGTTT
WI-7228b	254	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAAATTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTCTGCTTTGTAATCTATTTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAATAGAATGTTATCCAACATTAAGATATCTCAATGT
WI-7228a	163	G A	---			ATAGCTTCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAAATTCATAA TATGTTCCAGGAGATTACAATTTTGTCTCTTCTGCTTTGTAATCTATTTAGTTGATTTTAATTA CTTTCTGAATAACGGAAGGGATCAGAAG[AT]ATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAATAAGAATGTTATCCAACATTAAGATATCTCAA
WI-7233c	213	C T	---			CGATCGTACTGCCAGTAGCATTGTCTGTCTGCTGGCTGTTTGTACATTCATTTCAATTTGTACA GATGTGAACCTTTATCTCTGTCACTAATTAATTTAAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTTCTTCTGCCCACCTTTTGTGGCAATATTAAAGTGAAGTGAAGTGA GTGTAAGTA[CT]GTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG

WI-7233b	213	C T	---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTGTGTACATCCATTTCAATTGTTACA GATGTGAACATTATTCCTTGTCACTAATTATTTAAATATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTTCTTGTCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGTATC/TGTGCACAAAACCACTGCCAGATAACCCAGAGGGCCTG
WI-7233	211	T C	---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTGTGTACATCCATTTCAATTGTTACA GATGTGAACATTATTCCTTGTCACTAATTATTTAAATATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTTCTTGTCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAGT/CJACGTGCACAAAACCACTGCCAGATAACCCAGAGGGCCTG
WI-7238	128	T C	---	---	GGCTTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGT/T/CJCCGTT CTGTTTAAACAGAAAATAAAGGAGTGAAGTCTCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACAATTCAGTAGAACATTTTATTGCCTA
WI-7252f	520	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGGCCCCCTGCTCTGTGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252g	552	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGGCCCCCTGCTCTGTGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252d	540	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGGCCCCCTGCTCTGTGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252e	552	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGGCCCCCTGCTCTGTGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA
WI-7252b	540	T C	---	---	CCACGAGGATCCAGCCCAAGCGGCCCCCTCCCGCCCCCTCCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCCCTGGCTGGAGGCTGCCCGGGCCCCCTGCTCTGTGTCOG GACACTCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCCTCTCTCCA

WI-7252a	520 T C	CCACAGATCCAGCCCAAGCGGCCCTCCGCCCTCCCACTCGCAGACAGCGCGGGACAGAG GCCTGCCGGCGCGCCAGCCCGGCCCTGGCTCGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCOG GACACTCCTAGAGAACGCGAGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAAGTGGAACCTCAGTCACTTAGACTCCTCCTCCA
WI-7265m	252 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT/
WI-7265l	231 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCTTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT ATTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT TAAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT GTT ATAT TAT GTAA AATATA ACG CATCTCTT AAAA TACC ACAG TTTG TAT TTTT TCTTT /A/ AAG GAG TAAAG ATTG CCT
WI-7265e	227 T C	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT ATTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT TAAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT GTT ATAT TAT GTAA AATATA ACG CATCTCTT AAAA TACC ACAG TTTG TAT TTTT TCTTT /C/ CTT TAAG GAG TAAAG ATTG CCT
WI-7265d	174 T A	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT ATTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT TAAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT GTT /A/ TAT ATG TAA AATATA ACG CATCT CTT AAAA TACC ACAG TTTG TAT TTTT TCTTTAAG GAG TAAAG ATTG CCT
WI-7265c	170 T G	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT ATTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT TAAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT /G/ GTT TAT ATG TAA AATATA ACG CATCT CTT AAAA TACC ACAG TTTG TAT TTTT TCTTTAAG GAG TAAAG ATTG CCT
WI-7265b	121 T G	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT ATTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT GTTT AAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT GTT TAT ATG TAA AATATA ACG CATCT CTT AAAA TACC ACAG TTTG TAT TTTT TCTTTAAG GAG TAAAG ATTG CCT
WI-7265a	80 T A	AAC TTG GTT ATG TCG TCT CCG TGT GGT GAG CAG TAA GGA AAAAAA AGG CAT GCT ATG TGT TAC GTG TTT TTT CCA GTAT GTT /A/ TAT TTT GCC ACCAAAAA AGTAA ATG CATT TTT CAC CCATT CTG TGG TTT CATT GTAG TT GTTT AAG GAA ACCA AGC ATATAG ATG CATT AGT GATT TTT GTT TAT ATG TAA AATATA ACG CATCT CTT AAAA TACC ACAG TTTG TAT TTTT TCTTTAAG GAG TAAAG ATTG CCT
WI-7281b	183 C --	GAT CAC CCAG CCAAG CCG CTT CGAG GCG CTTAT ACC ATG GCG CAC CTTGG AGCAG AGAG CCAAGC ATCTT CCG TGG GAG TCTTT CTG GCG CAA GTCTG GCG CAG CCGTGG CCGTGCAG GTCTCC CATGAAGGCCA CCCC ATGG TCTGATGG CAGTGAAG CATCTCAG ACTCCTTGG CAAAAA ACGGAGTCCG CAGGCGCAG GTGTTGTAAG ACCACTCG TTTCTGTGG TGGGTCCTGCAAG AGGCCTCCTC
WI-7281	171 C A	GAT CAC CCAG CCAAG CCG CTT CGAG GCG CTTAT ACC ATG GCG CAC CTTGG AGCAG AGAG CCAAGC ATCTT CCG TGG GAG TCTTT CTG GCG CAA GTCTG GCG CAG CCGTGG CCGTGCAG GTCTCC CATGAAGGCCA CCCC ATGG TCTGATGG CAGTGAAG CATCTCAG ACTC /C/ AJT TGG CAAAAA ACGGAGTCCG CAGGCGC CAG GTGTTGTAAG ACCACTCG TTTCTGTGG TGGGTCCTGCAAG AGGCCT

WI-7282b	159	GC	---				TGTCACCTGGCACATTCTTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGTGAGTGTTCCCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTTCATAAAACCACAACTG/CJTAGCAAGATGCAAAATGCATGGCAAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAAAATCCACCAAGACAGTGCTGAGATTGG
WI-7292	92	TC	---				CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATATATCTCCCCACTCCACTAC TCTCTTCCCTCCACTTCAITTTCC/CJTTGTCTTCTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAACGATTTATGATATTTATGCTGTTTCTCTTCCCAATAGAAGATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTAGTTGGGCTGA
WI-7301f	133	AG	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	TG	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/CJTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	AG	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTG/CJGTAACTATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	AC	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	CT	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	GT	---				AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGGGGTATGGTGGTGGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGG/CJCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C	AACTATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGACCCAGGATATGGAA ACCAAGTGGTGGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATACAGTGGACAACAGCAATCA AATTACITGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49 G A	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/ATTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTAAACAAAACCTGTTTTT
WI-7314b	49 G A	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/ATTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTAAACAAAACCTGTTTTT
WI-7314	36 A G	CTCTCTTTTCTTCAGATCTGCTCCTGGGTTTAA/GJTITGGGAGGTCAAGTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTCTCTTTGCAGCAGTGAATAAAGTCAATTAATAAATTTCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTCTTCTGTGCACATGAACGCTTCTTTCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTAAACAAAACCTGTTTTT
WI-7321b	199 C T	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TJGTTGCTGGGTGTGGCAGCCACATCCAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCAACCATGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /TJGTTGCTGGGTGTGGCAGCCACATCCAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C	AGACATTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTGGGCACATGCTCAGGCTACTATAGTCCAGAAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATCTGAATTTGGGATTTTCAAAAGATAATTTTACATACACTGTATGT TATAGAATTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA/AC/CA
WI-7338c	221 A G	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTAAACTCTACCATGGATAATGCA AACAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAAACAAAGAAACAGAAATCAATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACAC/AGTATACACACAGACATCAGAAAATTTCTGTT

WI-7338b	125 A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGCAGAGAACAAAAGAAACAGAATCAATATATAAATCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACAGACATCAGAAAATTCTGTT
WI-7338	125 A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATAATTGGCAAAGGTGCTTTACCTTGAGC CATTATTTGTGCAGAGAACAAAAGAAACAGAATCAATATATAAATCAAAGACTATCTGCAGCTA GTGTTCTTCTTTACACAC[A/G]TATACACAGACATCAGAAAATTCTGTT
WI-7384c	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAATACCATTAATACATTTGTATTTCACTTGGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAATACCATTAATACATTTGTATTTCACTTGGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	CCTATGTCATGAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAAATACCATTAATACATTTGTATTTCACTTGGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGTCTCTGGCTGTCTGTAGCTGTTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGCTGTCTCCAGAAGCTTTTCCCCCAAGATGTATAGTTATTGG
WI-7388b	106 A T ---	---	TGAAATCCTGGTCTCTGGCTGTCTGTAGCTGTTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTTTGA CTTGCTGTCTCCAGAAGCTTTTCCCCCAAGATGTATAGTTATTGG

WI-7388	94 T A ...	---	TGAAATCCTGGGTCTCTGGCCTGTCTGTAGTGGTTATTTTACTTTGCCCCCTCCCCACTTTT TGAGATCCATCCTTTATCAAGAAGT[A]CTGAAGCGACTATAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGAACAAGTTACCTCTATTTGCCACAAGCGTCTGGGATTGTGTTGA CTTGCTGTCTGCCAAGAACTTTCCCCCAAGATGTGTATAGTTATGG
WI-7438	64 A G ...	---	TTAGATTTTAAATGGCAACCACTCACTGCCACCTTCCACTGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAACCTTATTGGAACCAAGTCTTCAGATTGNCCTGTGCAGACAGGTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAACATAGTTGTNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ...	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCTGTAGTCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT[C]GTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTGTCTACTTCTCAAAATGTTTTTGACA
WI-7454	152 T C ...	---	CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCTGTAGTCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT[C]GTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTGTCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177 G C ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCAAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTAAATTTCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7464b	168 C A ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCAAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATTAATTTTAAATTTCTATGTA CAACAGAGCCACAGCAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7464a	103 C A ...	---	AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCAAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGC[A/A]ACTAAATTAATTTTAAATTTCTAT GTACAACAGAGCCACAGCAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGAGCAACGTTCAACCAAAATTAT
WI-7499b	134 T G ...	---	CAATTCCTCAATCCAACCTAGTCTGNTGCCATAACCTTCCAGACAACCTCCACTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCAGAGGCACATCACGTTCTTTGAATGCTTCA[T /G]TATAGTCTCTTCATTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTAGGA ACTCTGTACAAAATCCCTTTGAAAATATAAAATTTTGGAATGAGTGATGA

WI-7499a	33 A G ...				CAATTCTCAATCCAACTAGTCTGNTGCCTAA[A/G]CATTCCAGACAAACTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTCTCTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAAATATAAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ...				TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGATGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ...				TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACCTTNAAGTAGTCTGGTCTGATTGCCTAGC[A/C]GGAGAGTTGAG TGCCACAGGTAAGATGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACCTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ...				TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATTGCT AAATTGT[C/T]GTGAAATAGGTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ...				TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGTTCTTGATGTTCCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATCCCGGTGATAGAAATTGCT /C/JAAATTTGCTGTAATAGGTAGAAATTTCTTTAAATATGTTTTCTTATTTCGTGAAAAATTCGG AGAGTGTCTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ...				GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTCTGCTT[G/A]GGAAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ...				GGGAAAGAAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCTGTTTGACAGGGAAGCCCCACTTGAAGGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCTCTCTTCTGCTT[G/A]GGAAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ...				GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/JCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAGGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG

WI-7555b	60	T C	...			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTCCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCAATCTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCAATTTGAATTTGAG
WI-7555	60	T C	...			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTCCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCAATCTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTCATTTGATGTGCAATTTGAATTTGAG
WI-7567b	290	G T	...			TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAACTTGCCTGGGCTGAGCATGAT GGGAATAGGGAGACAGGTAGGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCTTGG ATCGCTAAGCTGGCTGTTTGTGCTATTTATGCAAGTTAGGCTCTATGTTATAGGATGGGCTAC TCTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGTAAAGCTGGCTCTGTTT
WI-7569b	63	T C	...			AATGTATCCCTTTCGGTCCAAACAGGAAACCTGACTGGGCGAGTGAAGGAGGGATGGCA(T/C) AGCGTTATGTGTA AAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTGAATCCAT TGGACATTTGTAAGGCTTAATGAGTTTAGTGGAAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTTGATGATTCACCTTGATCATGCGCTACCGGAGGAGAGGAGTTG
WI-7574c	216	A G	...			GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G	...			GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G	...			GCCACAGCAGAATGGAGCGGTGTGAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAATCATTTTG TACCACCTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC(A/G)TCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T	...			AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAATTTTGAAGGGCGGTACTAGTTGACACACTTTGGAAGTTTGTGT TCTGTTTGTAAAACTGGCATCTGACACAAAAA(A/T)GTTGAAGGCCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGACAAAGCAAGCAANNNNNNNNNNAAGAAAAATAAAC

WI-7576b	168 A T ...	---	AATGATGATGATAATGATGATGACGACGACACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAAATJTGTTGAAGGCTTATTTACATTTTCACCTAC TTTGTAAAGTGAGAGAGACAAGCAAGCAAAANNNNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCAATCJCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACACGJATAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ...	---	AACCATGTTCCCTTCTTTCAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAATAA AGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCA/T/CJCAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50 G C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTTACAC/GJ/ATAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATC/GJ/CTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTT/CJ/ACTTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154 C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTT/CJ/ACGTAGGAAGAAGAGAGAGCATCAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTACACACCAAAATATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCATCAAATCGTCTCATCTTTCTCTGAGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTACACACCAAAATATCAAAACCCCAACATAAGTGTGCTTCCCTTAA AAATATGCATCAAATCGTCTCATCTTTCTCTGAG[GJA]GTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGCATCAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGATTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATAC ATGGCAGGAAGATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACATTA/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACAT TGGCAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCCCTTTTCCATTA/JCTTTTCCCTC TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCG/GTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	206 T G ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCT CGCT/GTTCCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCTCT CGCTTTCTTTTACACAGAAACAT/G/CACATACCGAGAAACCTATTTC
WI-7619f	237 G C ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ...			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGTGTCTCTCCCTTTTTCATCTTTTCTCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C ---	---	ACAAGGGGACCTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCC[G]CTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT[G]TCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[G]TTAAACCAATCATGGACCAAAATGTG CCATACTAATGATGAGCAATAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C]TJACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7626	144 T C ---	---	CCTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACCAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGGACCAAAATGTGCCA TACTAATGAT[C]GAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTCA
WI-7689c	134 A G ---	---	TCCCATACCCGCTGATTCTCAGGGTCTGTCTGCCGCCCAACCCAGATGGGGAAAGCAGAGTGGGC TTCCAGTGGCTGTGCCAGGCCCGCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTTCTCTAA[A] /GJTAAGGGGAGAGTCACACTGGGCAGCTGATACAAATTCAGACTGTGTAAAAGAGAGCTTAAT GATAATATTGGTGGCGCCACAAATAAAATGGATTATTAGAAATTCATAIGAC

WI-7689b	134 A G	TCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAGGTTGTTCTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCACAATAAAATGGATTATTAGAATTTTCATATGAC
WI-7689	121 G A	TCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAGGTTGTTCTCTAAAJA AATAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGGCACAATAAAATGGATTATTAGAATTTTCATATGAC
WI-7690	45 G A	TGGAGAACATTCAATCTTCCGTCACATTCATCAATGAAGATTAGJACACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCCAGCATGTTAGTGGCAAAGAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164 T C	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAATTCJGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	158 T C	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTCJAAAGTAAATGGTCTCTCAGTTGTTTATTTAACCTCTAAATTCT TTCATTTAGGGGTAGCATTTGTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A	TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACJCAJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGAGCCTCATCCGAGGCGGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275 C T	TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACJCAJCCAGGAGTCCCTGGTAATAAGTACT TACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGAGCCTCATCCGAGGCGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCCAAACG
WI-7743e	106 C A	TAAATGAGTGTGTTTGTACCCGTTGGGATTGGGAAGACTGTGGCTGCTGGCAGTTGGAGCCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACJCAJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGCTACCTCAGTGGGTCTCTGGGGCTCGAGCCTCATCCGAGGCGGGTCAGGA GAGGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743d	275 C T ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743b	275 C T ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGGCC
WI-7743	275 C T ---	---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCAGCACTAAAGCAGTGGAGCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACATTACAGAAATTATGAAGAGGTATCTGTTTAAACATTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC/GJTAGTTTAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAATGTGTAATTTTGTATATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126 GC	ACAGGCGCTTTGGCAGGTGCAGCCCCCACTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAATTCCTCTCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAAACATTCOCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTGCCACCCCTCATGCTGTGTGACTCAAAACCAATCACTGAACCTTGCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237 CG	TTAATTTACTGATTCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTTGATAAAGATTTCCTATTCCTTGGTCTGTGAGAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGTTCAATGTCTTTTACCCCTTNNNNNNNNNTTGTAAAGTCTAGTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAAGC/GTTTTTCGACGTTTGA
WI-7774b	170 TC	TGCAACCTCTTTTCGTGATGGGCGCCTGCTGGTCAGCACTCCAGTAGCGAGAGAGCGGACCCAGAATCAGATCCAGCTTCGGCATTGTATCAGACCAACAGTGTGTTCCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTGCAGGCACCACCTTTAATCTGTTT[C]ATACCTTGCTTTAATAATGAGCGACTTAAA ATGATTGAAAATAATGCTGTCCTTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165 G --	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGTATTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785b	165 G --	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGTATTATTTTGTAAATGTATCTTGGTGCTGC
WI-7785	156 - T	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATCTGTAAATGCATTGGAATAAACTGTCTCCGCCATTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNI- /TNNNNNNNGCCAAAGGCTAATCCAATTATTATTCACATTTACCATAATTTATTTGTCCATTGA TGTATTTATTTGTAAATGTATCTTGGTG
WI-7789c	84 GA	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATTCTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84 GA	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATTCTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTAGGGTCCCTAAAAGCATTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ...	---	TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGACCACCTCTTACAGAGACTCTCCC TGACG(G/A)GTGGAATTTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCGCTGCOCTAGGATAT GCCCTCCTGGTGAAGTGGGGCTGTCTCAGAGACTAGCCAGGACCCATCT
WI-7790b	190 CT ...	---	AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTCCTAAGGTACTCTTCATGAGATTCCATT TACTAATAGTGTATTTTGGTGACTAGGCTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAAGTTGTGTTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7780	190 CT ...	---	AATTGTCAGTCACCTCTTCAAACCTTACAGTCTTCTCCTAAGGTACTCTTCATGAGATTCCATT TACTAATAGTGTATTTTGGTGACTAGGCTGCCTATGTGCTTATGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAAAGTTGTGTTCTATTTCTTGAAGTCTC/TJTTCTATACTTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81 CA ...	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A/G)TCATCATCAAGAAATTTAATGATTAAATAGCATGCCTTTCTCTCTCTCT TAATAAGCCACACATATAAATGACTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ...	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTTCAT CTTGATGATGATC(A/G)TCATCATCAAGAAATTTAATGATTAAATAGCATGCCTTTCTCTCTCTCT TAATAAGCCACACATATAAATGACTTTTCTCCAGAAAAATTCCTTGAGGAAAAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ...	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(G/A)TTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ...	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG(G/A)TTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ...	---	TTCTCTCATTTTATCCCTCACCTGT(A/G)CATGCCAGTCCGTTTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTTTAGAGAAGTATACATAAGTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTTAAAGAAATAACAGAA

WI-7830d	150	C T	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTTGTTTGTGTCACATTTTACTTTTTGCGTGTGGA
WI-7830c	54	G A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTTGTTTGTGTCACATTTTACTTTTTGCGTGTGGA
WI-7830b	134	G A	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC[G/A]ATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTTGTTTGTGTCACATTTTACTTTTTGCGTGTGGA
WI-7830	44	A G	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTCCCTTTG AGTTGATCGTTGTTGTTTGTGTCACATTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGAGGCAATTTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T ...				CCACTTCTATCTGATTTTCCAGIC/TJAATGAGGAGGCAATCTAGTCTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTAGGGTGTCTTCCAACCTGAAATCTCAATGTTCTCAGTAGGAAAC CTGAAATCACATGCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ...				CCACTTCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTAGGGTGTCTTCCAACCTGAAATCTCAATGTTCTCAGTA/C/TGAAAAAC CTGAAATCACATGCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ...				TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCAGTCTCCCC CTAACAATTACCCTGTCAAGAGG/C/GAGTGCAGCTCAGGTGGATTTAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ...				TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTACCCCTCAGCCTCAGTCTCCCC CTAACAATTACCCTGTCAAGAGG/C/GAGTGCAGCTCAGGTGGATTTAATGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTTAAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTGCTATAAATCTATGT CTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ...				TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CAITTTAATTTCCCTGTCTTACCCCTATTCAAGCA/C/TJTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T ...				TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT CACCCAACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CAITTTAATTTCCCTGTCTTACCCCTATTCAAGCA/C/TJTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C ...				TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGCTTT /C/TJACCCCACTGCTCCCTCTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCAITTTAATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85 T C ...				ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGTGGCGGGAATCC/T/JATTTATCAGACTCTGTAATTAATTAATTAATGTTTACTCAGAGGA GCTGCAAAATGGCTGCAAAATGAAATCCAATGAGCACTAGATAATTTAAACATCATTAATGCCC CITTTATCAAGAGCACATCAATTACAAGCTGTAGACCCTAATATCAATTTG

WI-7870	76 C T	---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAAGAACACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGCGC/TGGGAATCCTATTTATCAGACTCTGTAAATGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATCAATTTG
WI-7889c	54 C	---	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C	---	---	---	TTAGTCTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGGGCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCTGGAGAGGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G	---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC/A/GTATGTAAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G	---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGTCCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC/A/GTATGTAAATTTGCAATTTTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTATTTCTGAGCTAAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTATTTCTGAGCTAAAACCTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T	---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/CCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTTATTTCTGAGCTAAAACCTCAACTATAGAAGACATTTAAAGAAATC

WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACAACTCCAGGCCCTTGGTTGCGGCTGCTGGTTATTGGGCGAGCGCGCGTGGTCT CACTCAGTCGCTGCTGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACAACTCCAGGCCCTTGGTTGCGGCTGCTGGTTATTGGGCGAGCGCGCGTGGTCT CACTCAGTCGCTGCTGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT

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WI-8021b	57 C T ---	---	ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/CTGTGATCCC ACGCTTTAGAACCTTCAACACAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCCTTTACACTTTGAGATTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57 C T ---	---	ACAACTCAGAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAAC/CTGTGATCCC ACGCTTTAGAACCTTCAACACAGGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCCTTTACACTTTGAGATTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	208 A G ---	---	CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCAATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGCGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAAACCATTTTCAAGCGCTCTAGCCTCTAA TTCCCA/GJCTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCAATTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGCGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAAACCATTTTCAAGCGCTCTAGCCTCTAA TTCCCA/GJCTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAAAGGAAAGAGC
WI-8077	167 A G ---	---	GAATGAGCCTTCTAGCGCCGAGGACCTGCTGCTGTTGGCTGCACATGCATTCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNINATCGCCCAACTCCTTTCT AAGGAGCTGGGGTGTATGCCCTACAAACC/A/GJTAATCTCATCAGATGGATTTTATTTAACGTT GTGATTTGTGACTTACTTTCCAACTGACTCTGGCATAACAAAGGGAAGAA
WI-8118f	114 GC ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTG/GJTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTGTTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAATACAGAATGAGCTTGTGTTTT/GJCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T	---	---	TCTAGGTTTAATCAAGCAATTGCANTTTGGAATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGAAACTGGCAATACAGAAATGAGCTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C	---	---	TCTAGGTTTAATCAAGCAATTGCANTTTGGAATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGAAACT/C/GGCAATACAGAAATGAGCTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T	---	---	TTTTCTCTCCCGGGGACCAAGGTACCTTCTGGGGCATACAATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAAGTGGCAAGAGCACAAATGAAGAGGATGATATAAAACAATCACGGCA
WI-8171c	46 A G	---	---	TTTTCTCTCCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCAC
WI-8171a	46 A G	---	---	TTTTCTCTCCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/A/GTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCAC
WI-8171b	298 T C	---	---	TTTTCTCTCCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCACGGCA
WI-8314b	85 G C	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/C/GAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78 C G	---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/C/GTAAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCAGCTGTCCAATAGAATTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

WI-8321	178 G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCTTAGATAATAGTGCACCTTTTTCAGTATGTTCCAGATG/GA/JAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8321	178 G A ---	---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCTTAGATAATAGTGCACCTTTTTCAGTATGTTCCAGATG/GA/JAGTATCTTAGTATCTTTCTA TTTTGCTATGGTTCTAGTTTATCAACCTACTTTTATTAGCTGAACGTGTGGC
WI-8332b	123 A C ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTTCCCTGTGCAGCCTTAGA/JC/JACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 A C ---	---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTTCCCTTCCCTGTGC/JC/JGCTTAGAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCTACTGCAGCTACTTAGTAACAACCTAG AGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACTNTCACCAGGCCCCCTCCTCCAAACACGTGGGG
WI-8378	308 T C ---	---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTCACATGGCAGCAGGAGAAAGAGAAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCAGTGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACTNTCACCAGGCCCCCTCCTCCAAACACGTGGGG
WI-8426	184 T G ---	---	---	TTTAGCACATTTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTTGTGTGGANGGGGTGCTTGTCTGAACTTCCATTCTGT/GT/GCCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCGGGGCCCTTGGCNATGNATTAGTGAG
WI-8450h	61 C A ---	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGCCCTTCTACATACACTC/A/JCA TCTTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATTATACCAATCCATTGTTATTTAAGA AAAAACCTCCAGTTATGTGCAGAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTC/JTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ...			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/CJACACTCCAT CTTCTCTATCTTAGTCCAAAGTTTATGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ...			CAAGGAAAGCTGTCAGTCTTCATAAATCTTCAAGAGTACAAAAATACGTATTTTAA/JGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATGTTTAACTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTTAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A]NNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAATGCCAA TTAGACAAAAGAGANTAAATGATATAATAATAATCATTTTTTNNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A]NNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATAATCATTTTTT[A]NNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGTAGTACCTTAATTTTGATAAAAAAAT TAAAAAGCAT[A]G/AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTCCCTTTGTTTTGCTTTTTAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAATCCCAGTCTGCAGCTCAGTACCTGTGTC/TGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAAATTGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAT[C]TCCAGTCTGCAGCTCAGTACCTGTGTCGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGAGGGTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTTGACCTGTAAAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAGANCATTA TAAAAAAAT[C]CCTCTAAAGNGACACATGCCCAAAATGACCAANGNCATGAAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTNCCCTACTNTTATCACTGTGCTCTGCTCTGCTGCTACCTA TGNGAACTGCACACTATCTGCGCAATATGT

WI-9446	75	T C	---			GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCACTCCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCCTAAAGNGACACATGCCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGCTCTGCTCTTTTGCTACCTA TGNGAACTGCACACTATCTGGGCAATATGT
WI-9497b	185	A	---			ATTAAGTGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAACAGTCTCCAAATTTTNCCTTAATTAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185	A	---			ATTAAGTGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATCTAGATCCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAACAGTCTCCAAATTTTNCCTTAATTAATCAAGTATGTTAATGTCACCT GGAATCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193	C A	---			GTGAAAAAGTTTCTATTCCATCCATCACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAAATTACAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTGTAC/AJAGTG AAAGCTCTTCAGCTTGGAAACAACTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A	---			GTGAAAAAGTTTCTATTCCATCCATCACAATAGATTGTGCTAAGGATCATTTTGGAAAGAT GTGAGCATTCAGAAAGTTGTATCTCATGTCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAAATTACAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C	---			AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAAGTATTACCAGAC AAGCATCAGTGATGTATAGTCCCTTTCAGTTTGTATTGTACAATGCTGTAGATAATGCGCCCATG CAATACACCCCAAGAACACTAGAGTCCCTACACCCCAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GT/CJGCTGGATACCACTAAGAAGTCTACTGCGCCCATGTTGGTTATGATTT
WI-9555	97	G A	---			CCAAAGCCCAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTTGAGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/CJG/CTTGAATAATCAATTCAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTTNCCTCAGATTGATCACA
WI-9625b	172	A T	---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAAACTTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTTCT/ATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAAAGGTTGTGGACAAGTTACTCTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T	TTTTCTGAGATCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAGCT TACAACT[C/T]GTCCCTTTACCTGATACATTTATTCATTTACTTTCACTTTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCA[A/G]GATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676m	184 G T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGC[G/T]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676l	84 A C	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676k	202 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/T]CAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676j	92 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT
WI-9676i	173 T C	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTGTTT

WI-9676h	134 C A	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC C/AJATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJCAAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184 G T	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCG[GT]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173 T C	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134 C A	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAJAGJGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114 A G	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAJAGJGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92 C T	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84 A C	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAATTTGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTCACATATGTGAGTATCTA TCITTTATTTCTGTCCTTATGTTGGTGGCACATGCTGTGATTGCTGTCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACCTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTCACATATGTGAGTATCTA TCITTTATTTCTGTCCTTATGTTGGTGGCACATGCTGTGATTGCTGTCC
WI-9756	47 A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAAGTTAATCTGTGGAAAA GAGTAACTACAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGGTATCCACTCCACAAACACAGAAATATACACTTTTGGGAA ATTCCACTTAACCACTTGATCTTCACCTTTTATGATTTAAACCTCTCCGTGG
WI-9758	135 A G ---	---	GATGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAGAGAAATCTTGTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAATAAATCTGTGAGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTCTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACCTTTCATATGCTCTGTACCCAACTATAAACTTTTG GTTCTCATGCACCATTTTCATTTTGCTTCTCCTCAAGTACCACCTGATTTTACCAATTT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTTGGCTCCTCATGCGCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTGCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTT[C/A]TGGATCCCACCCAGGA CTCAAAAACCTAGGAATGGGAGAGAGGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATATCTTATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAAGGATAAACTAAGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGGATGTTACTTGATGCTGTTG
WI-9880c	222 G A ---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAAACAATAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTTAGACCAATAGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAATTTATATTTATAAGCACATGAA AATGGAATGAATAATGA[G/A]TTGACATAGGAATACCTACATATTTTG

WI-9880b	157	C A	---				GAACAAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C/A]TATATAAGATCCTCTTTAAAATTATATTTATATAAGCACAT GAAATGGAATGAAATATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---				GAACAAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAAATTATATTTATATAAGCACAT GAAATGGAATGAAATATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---				ACACTGAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCAAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAAGAGCTACACAAAATTTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGTCAATGAATATGATTCCTCAA
FB25G10b	109	A G	---				TCCCTCAATGACAGATGAACATAATTTTCTCTGGGTAAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGAATTTAGATCCTCCCCCAG TGACAAGTAACTGAACGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G	---				TCCCTCAATGACAGATGAACATAATTTTCTCTGGGTAAGAAATACCTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGAATTTAGATCCTCCCCCAG TGACAAGTAACTGAACGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A	---				ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAAAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTATAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTCCTAAACCCCTAATGAGATTTCACCTGGNCTCAAGTCATTTTGTAGTGA GGCATTCAATATGACCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T	---				CGTCTTTCCTTTTGGATTTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGTTGTCCC TACTGAGCTTGGGCCAGGTGTGTACTTAGGAACCCCAATCCCAAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAGCTTGCC
S72904	51	G T	---				AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTTCCTTT[G/T]AATTTGTGAGTTC ATTCCTGGAATAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTCCTCAAAACCAAGTGCTGAACCTTCTCCCTTTCTGTCATTTGGTTGCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTGGAGTGTTTCAGTGCTGTGA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTTGGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACTTTAGGACACACACACAAACACAGAGC/TJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACCTTCCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGACACAGTGTGCTGACAAAGGTGACACTGAACANAAACAGTTTCTCTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAAGTTCTCTATCACAAATTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCCGCCAGGCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAAGTGG
ESTC129	20	---	---	---	AGTCACCATGCCCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAAAATGAACANGAGAAGCTGAAACAAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGTCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGTCAAGTTCAGAGAGGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGTCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTTAAATC AAAGANACCATTCCATTTCCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGAGGGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACCTTTGGTTTAAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGGCCCCATTTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAAATT ATATTATTGATACAACTCATGAGCATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCCTGGCTGCCTGGGATGGAGCGGGGGCGCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	TTTAGCATTGGTGGTGAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACTGGGCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTCGTCCGTTTGAAGTTGCTGTTTGTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATATTGGTTTTGTAAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTGGATTAGAGGAAAGTGCCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAATTTTNCITTTATTTCTATTAAATACCTTTTAT TCTCTTTATTCOCATAAAAGGCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCCTGACAGTCCCTTCCCTGCAGGGGCCCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTCACAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAATTTATAAAGTGCCAGATNAGTGCTAATTGTCAATCAGCTTG ATTTTCACTCA
ESTC187	24	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATGCCACGAGAGACTGGATGCCAAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTACACCCNTGTCAACCTCAAAACAGATGATACATCATCACTTGCTTCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCAGACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAAATACCACTTCCCTTAACCTTATCAGTCTAGTAAGCNTTCAAAGGAGGAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNGCAAAGTCTCCCAACAGACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGTATAGTAAAGCTCTGNGGAATCCAAAGATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCTTTTGCCTGCAACAG

ESTC201	35	TCCTACTTGGGTAGTTTAGCAAAACATTTTTAAAAACCACATCCACAGATTGGTT
ESTC202	22	CTGCTGGAGGGAGACAGACGGNCAGGGCGCTGGGTGGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	ACACTTAACAGGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGTAAGATTTTATTGTGTACTAC AAGACACGTTGCA
ESTC208	43	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAAAGC CTAAGAGTGAAAA
ESTC210	29	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAGTGACGGTGACCTGTG
ESTC212	27	GGGTAACTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	CTCAGAGTCCTCTCTCANACCAGGGCAGGGAGTTAGGGAAT
ESTC216	49	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAACAAGTTTCAT AAACACACCCCA
ESTC219	32	GTACACATCTCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	TCATTGAAGAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	TGCACTGTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAAGAGCATAAGTGCTTCAGAAGGA ATGTGATAGATCG
ESTC23	27	TTCTACTTTATTTCATATCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	GCCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	CAAAAGGGTAGTCATATTTCCCCANCAACAGCATGATAAAAATAATTCAC

ESTC28	23	GAAGAGCTGGGCACGCATCTGACNTTCTTCCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	CAGACATGACCTACCGTCCCGGCCCTCAATTCATATTTTATTCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACATCC
ESTC31	32	ACAGCCCCACAGAACTATTGTAAACAATATTNTCAGTGGTGATCATTTGTAATATACAAATACAAAG CAATTTCTCAGA
ESTC33	25	AGCACTTCCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	AAGGAAAGGGAACCCACCTGGGCTTNGGTACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAGAAACCAATT
ESTC40	22	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAACTCTCATCATCGAGGCTATATATAA
ESTC50	56	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGCCAGGAGCCACTGGTGGGANCCTGGCAGATG TTTACCCTGT
ESTC56	45	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGCAGGTCGGCAGGAAGNAGTGGAGGAAAGGACACCA AGT
ESTC57	20	AAGTGGCCCTCCAGTCCCNCTCTCTGGGCACAGATCCACCACTCTGCTC
ESTC59	38	GAAACACAAAAGTGTGAGAAAAAACTCTCAAAATNGTTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAATGCATTATG TGGACTGAACCG
ESTC61	57	AGTGATTTGGCTAGGCGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	ACAGACACAGCATCACACCANAGGGCCACCGGGAGGGTCCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTAAATCCCCACACTTACTTACTGCTCATCCGT CACITTCGCTAA
ESTC7	45	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACT G

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCNTTTGGCGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAATCAAAATATTCATCAGNTTGGGTTGAAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTCCTGTCCCATCGGAACACAGAGTTTCCCCAGGNGAGCCCTTCCCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGTTGGGAGGCTACAGCCTGACCCACATTG TTTGC
ESTC83	53	---	---	---	ATTGCAAGGAAGTGAACGTGNTCAACACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCTCTCGTCTGGCATTGGCTCTCCTCCTCNGGCCAGTGCTCCACCCAAAGTGCTTCCCGATGAT
ESTC89	22	---	---	---	CTCCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGCGAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCCTCTCCAGAAGTTGNAGACGTCTATTTAGTTTGATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGACTGTCTCCA/C/TJGCCAG ATTCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTTCACAAAATCAAAAAGAAAGAAAGGCTTAGCTG
ESTC95	32	---	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTGTTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC/A/GJGCCCTATTACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-100	127	C T	---	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCAATATCATGCCAGCTTCTGTGATATGATGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG/CITGGGAAACCAAGCCCTATCTGAGTCTTGGCTCCCTCC
DWU-177	77	A G	---	---	
DWU-286	213	A C	---	---	

DWU-252	94 A G ---	---	---	AGTATACAAACATTTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCCTCA/GJTGAGCATGGTACTTGGCCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCCTATTGATTTAAGCTTCCTGTTGAATGACAAAGTATGTGGTTTGTGA AT
DWU-330	85 C T ---	---	---	GAACATTCCTCTGCAGCACITTCACCTACCAATGAGCATTAGCTACTTTTCAGAAATGAAGGAGAAAA TGCAATTATGTGGACTGA/CJTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTTCCCTTTTGCAA CAAGACAAGCAAAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATTGAATGTGTTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	---	GAAATGTTAATTGGCGAGTGAAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAAGCCAGCTGAAGAGTAAAGGAAAAAGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGGCCCTTCACCTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCTC/JAG/CATCTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	---	CTCTTAACCTCAGTTCCTCATCTATAGAATAAGGGATTGAGTTGTGATCACATAGCTCAGGTAATC CAGGACAGAAAACCCAGGAGC/JAGTGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	---	CTCTTAACCTCAGTTCCTCATCTATAGAATAAGGGATTGAGTTGTGATCA/CJTATAGCTCAGGTA ATCCAGGACAGAAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCTCTCCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTG/C/GJAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTC
ESTD-ADAA	184 G A ---	---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCTCTCCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAGTGGGACTGTGAGGACATGGAGCCCTC/JAGJCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGTCTTGCTC
ESTD-ANT1	160 T C ---	---	---	TCTCTGTCA/TTCCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATTC TGGACTGCCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTACCTT TTTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398b	168 A G ---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTTGATGATGTTCAATTTGGGGCTTGACTTTCCAACACGGAGAAG CATTTGTTTCTTCGGGCCAAGAGGTATCTACCIAGTATGTTGCTATTAGGCATTG

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EST10398 2a	147 C T	TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTCAACATTTGGGGCTTGACITTTCCAAACACGGAGAAG CATTTGTTTCTTCTCTGGGCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTTG
ESTD-C7	14 G C	ATATCGTGGCCTTAG/CJTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C	CTTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACATTTCAAGG ATAATGGGCAATCACITTTCTTTT/CJCTTCTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A	AGTCTTCATCTCGGGTGTCCAGGTAGATCCCTTTTACC/CJACCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G	CTGGGCTGCGCGCAGCAGCTGCTGGACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGTG TATTCGTCCACAA/A/GJTGCACTGGATCAGCT
ESTD- HRASa	37 C T	CTGGGCTGCGCGCAGCAGCTGCTGGCAOCTGGACGG/CJGGCGCCAGGCTCAOCTCTATAGTGGGG TCGTATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G	GGAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGACAGAGAGCGGCCTCAGTG TATCCCAACCCCA/A/GJTGCGCGCTGGAGATGAAGAGGATGATGCAGGT
ESTD-OTC	18 A G	GTGACCTTCTCCTTTAA/A/GJAAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAACA
EST36751 7	36 C T	CCAAAGTGTTCATTTAGCTTTGCAGGTTTAACT/CJGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562 3	109 A G	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAAT/A/GJTTTACCTTTGAAAAATAA ATGAAGGATTTGACCTGCTCGCTCTGGAAAGATATCCGTACCGTCTGACGTTTGAACAATACA GATGCCCTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	121 C T	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGCTCCCTGA/CJGGGAGCCAGT GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T	GGGAGTGACAGCTAGAGCACCAAGGGGGGCT/CJTACAGCTGTGTCTCATGGAGGACAGGCTTCT GCTCATTTCTGG
ESTD-ALB	180 A G	AATCCAGCACTTTAGGAGGCTAGGCAGGCATATCACAGAGGTCAAGGTTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGAGGCG/A/GJAGGTTGTGGTGAGCCGA GATGGCAOCCATTGCACCTCCAGCCTGGGCAACAAAGAGTAAACTCTGTCTTC

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EST70523 3	182	GT	---			TTCCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGGCCACCCCGGGCAGCTACCGCTCT CGCTCTCGGTAAACATCCGGCCGGCCGCTCTTGAACACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
ESTD- APOA2	101	CT	---			CCAGGTGTTGTGCACGCTGCCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGGAGGGGAGGTTGCAGTGAGCTGACATGCTGCTGCCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	CT	---			CAGTGTATCTGGAAGCCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTGAGCATCTTTGGCTCATGAAGGCCAAATCCGAGAGACCTCTAGAAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTGTGAGGCCAGGTTTATA GCACACTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCCTT
EST74167 6	137	C	---			AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACTGGAGGAACAACCTGACCCGGTGGCGGAGG AGACCGGGCAACGGCTGTCCAGGAGCTGCAGGGCGGCGAGGCCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCCGCTGTGTGAGTACCGGGCGAGGTGCAGGCCATGCTGGCCAGAGCAACCGAGGAGC TGCGGGTGGCTCGCTCCACCTGCCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132	C	---			CGCTGTGTCAGTACCGCGCGAGTGCAGGCCATGCTCGGCCAGAGACCGAGGAGCTGCGGGTGCG CCTCGCTCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAGCGCC TGGCAGTGTACAGGCGGGCGCGGAGGCGCGAGCGGCTCAGCGCCATCCGCGAGCGCTG GGGCCCCGTGTGGAACAGGGCGCGCTGCGGGCGCGCCACTGTGGGCTC
ESTD- AFSB	126	A	---			GGAAGAAATGGAGCCTGTGGAGGAGGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCCCTTCTGA AGCAGAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCATCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C	---			TGTAGCCAAAGTCACTGCATCATCATTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCCAAATATACTGGGTTTCCCTGTTTCCCTTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAAGGCCCTAAAGAGGCTTATG
EST26021 1	137	A	---			TAATGTAAGCTCATCCACCAAGAGCCCTGCACCATGTTTGGAGTTGAGTGACATGTCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATCTCTGCAGCACTTCACTACCAAAATGA GCATTAGCTACTTTTCAGAAATGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTCTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A	G	---		GGCAACATAGTGAACCCCATCTCTACA/G/AAATACAAAAATAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCACGCTACTTGGAGGCTGAAGTGGGAGGATCCCTAAGCCCTGGGAGGTGGAGGCTG CAGTGAGCCCAAGATGTGGCACTGCA

ESTD- BCL2	116 A G ---				AGCTGGATTATAACTCCTCTTCTTCTCTGGGGCCGCTGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGATGGCGACGCTGGGAGAC/A/GGGGTACGACAACCGGG AGATAGTGAAGTACATCCATTATAAGCTGTCGACAGGGGCTACGAGTGGGATCGGGGAGATGT GGGCGCGCGCCCCGGGGCGCGCCCCGCAACCGGCATCTTCTCTCCCA
ESTD- BCR	69 C T ---				CAGTGGCTAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGAGACTCATCATCTGCGCAAGA GA/C/TCAAAGAGGTGAGCTTCTGTTGTCGGGAAAGGAGGAGGAGCTAAGCTAACTCTGCTTC AAATCAACCATCCGTTGGACACTGTGTGGCTGCCATCTGCCTGGCACA
ESTD- BRCA1a	119 C T ---				AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGATGACGATTTCA/C/TJGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTGTTACTTGAAGTAGCACTAGGGAAGGCAAAAAACA GAACCAATAAAT
ESTD- BRCA1b	139 A G ---				ACTAAATGAAGAAATCTGTAGAGGAAACCTTTGAGGAACATTCAATGTCACTGCAAGAGAA ATGGAAATGAGAAACATCCAAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAATGTT TTTAAAGIAGIAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD- BRCA1c	126 A G ---				ATGCATCTCAGGTTTGTCTGAGACACCTGATACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGTAAGATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA/A/GIAGGA GAGCTTAGCAGGAGTCTAGCCCTTACCCATACACATTGGCTCAGGTTACCGAAGAGGGGCA AGAAATTAGAGTCTCTAGAAGAGAACTTATCTAGTGAAGATGAAGAGCTTCCC
EST51212 0	122 A C ---				ATCTGAGCTCGCCAATAAGCTTCTGGTTCTACTCTCTCTCCACAAGCCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---				ACACAGTGTCTGGCACTGGGGCTGGGATCCTCCTCCCT/A/GJATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---				ACACAGTGTCTGGCACTGGGGCTGGGATCCTCCTCCCT/A/GJATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---				CCCAGTCAGTTGGGGACAGCCATGCACGTG/A/CJGCTCTGTGTAGCCTTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---				GTCCGAATCCTCCTCCTGAAAGTGGCCGGTTAATGTCTCATGACGCTGCGGCTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACCGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAACTCCCTTGAAGCTGGGAGTGGGTTTAGGACCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67 A G ---				ACAATCCAGGTACACATTCAGAAAGAGGAGGGGTGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA I/A/GIAGATTACGGAAGGAGGCCACGAGGATCGAAAGTTAGTGAAGTC

ESTD- CB22	119 C T	GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGAGTGCACCAATAGG[C/T]GATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACAC
ESTD- CB23	136 C	TAGAACCATCAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCGGCTTCTCTCACACATACAGAGCCCTACAGGACACAGACGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTGTTCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145 A	ACCGGACACAGACGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGTGTTCCACCCGAGGTGGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTACCCCGACCACTGGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGAGGAGGACACACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G	GTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTTCGCCGTC TCTGCTCTCGAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTA/GTCTACATGCTGTCTTGTGTAACAGAGTCTTACAGAGGGGTCTGTCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTGTATGCGGTG
ESTD- CB27	125 C T	TTTTCTGTTTCCCTGAAGATTGAGTCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGTTGCATTTGAGGAGTGTCTGTGGAGTTCTGCTCATCACTGAC[C/T]TATCTTC TGATTAGGGAAGCAGCATTCCTTGACATCTGAAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCAACACCACTTCCATACC
ESTD- D4S338	59 A T	TTTTCTGTTTACCTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TJATGTA TTTCTTAAACAATAAATGAAAGTCCAAATTAATCTCTGATCCATGGAAGTGCAGAAATAAATGTTA TTTTAGCTGTGAGAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTTCATGCAGTAG
ESTD- CYP2D6	61 A G	CAGGCGAGCGTGGTGGTGGTCCATCCCGGAGAGAACAGGTACGCCACCACTATG[C/A]GJCA GGTCTCATCATTTGAAGTGTCTCAGGGTTCCCTTGGCCTGAGCAGGCGGAGAGCATACTCGG
ESTD- D11S1873	40 A C	AAAAAACAATTTTAAACCTTTTCAATCATATACACCATATG/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATCTTGCAATCTAAAATGTCAATGATTAATGCAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTGTAGTCCATGGAAAGGCTCTCTCTGGGGCGGTG GGGTGTGGCTATGTGGTGTCTGTGTAGAC/TJGGGGGCTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC

ESTD- D17S33a	75 C T	CATCCCAAGCCCATCTCTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTGTAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGGTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G	TTTGAGACCACCTGGCCAAATGGCGAAATCACATCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCATCGTAATCCAGCTACATCGGAGGCTGAGCGAGGAATTGCTTGAACCC(A /G)GAGGCGAGAGCTTGCAGTGAGCCAAAGATCACACCTTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTAATAAGAAATTAACAGAAATATCATTTG TTATCCAACTATTATCACTTATTTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G	AGGTTCCACATTATGCTGATGTTTCTGATGTTTCC(A/G)GGAGCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAACTCTCTACAGCCGTTGTTGTTATTAAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCCTGC TGAGTCTTATTCAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATAGTGTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGTCTTATTGGAAGGATGCCGTTATGT
ESTD- D3S2a	248 G	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCCTGC TGAGTCTTATTCAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAAGTGAACATACCTGCTCCTAGAACCCAGAGTCATAGTGTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATACTGTCTTATTGGAAGGATGCCGTTATGT
ESTD- D7S399	83 A G	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC(A/G)GTCTCTCTACATCTCTTTCACAAACATTTTCATCCATGGACTCCATAG TAGAATATTGAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGAGACA GAATGCTGATT(A/C)TCTGGTGGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGCAGCTGCTTCCAAG ACCTCCTGATTGAGGAAGGGAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCTCC(A/C) GTTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGAGA CAGAACTGCTGATTATCTGGTGGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGCAGCTGCTTCCAAGA CCTCCTGATTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT

ESTD- DRD1	154 C T	TCCCAGCCCTATCGGTCAATGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTGCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCCTTCGGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C	TCTGCCCTTGGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGGTACAGCCCCATCCACCCAGCCACCACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCCGCCAAACAGAGAAGATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTGGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T	AAGACGATGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGAGCATGTGGCGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGATGTTCAAGTGGCCTCTACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGAGGTGCGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB82	93 C T	TCTTTCAGGATCCGATCTGCGCTGGTTGGGCATGCGCTCGCTAGGTGTACGCGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGCGCTGGGGCGGGTGCAGACCCAGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCCGTTCTCTGACGAGTCTCCGCTATGTTACT
ESTD- ETS2	43 A G	ACTCACAGTGCTTTAAGTGAAATGGTCGAGAAAGAGGACCCAGTGGGAAGCCGCTCTGGCGCCTG GCAGTCGGTGGACGGGATGGTCTGGCTGTTGAGATCTCAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACCAGGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTTTCAGAAAGTTAGTTG
ESTD-F9	111 A G	AGATCCTGATGATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTATGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAGTATGATGTTTAA/GTGTCAAACTTCATTTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATACACAAGGAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACATTTTCGAACACATTGAAGTTGTTTTGAACTTGGTGTACACCTTTAATTACAACTAG CAGACGGAACTGAACCTCAGGGTAAGAAT
ESTD- G00H	200 C G	CGCAGACCGGTGAGTGGGGTGGGAGTGTGAGGGAAGGAGGGGAACTGGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAGGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTTACAGCTGTCTGTCTGCCGAGTTC/ G/GACTCTGTCCCGAAATTCGAGAGCT
ESTD-GCK	88 A G	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTCAGGAAGTACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGGGCTGAGCCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGGTCAACAG

EST34088 2	62 A T	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAAGAGACCGGCTC[A/T] AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCAC[A/G]GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G	GGGCTAAATTTCCGAGCAACTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT5	149 C	AACACACAAGCCCCAGCGAGAATTGAACCTCGCGACCCCTGGTTTACAAGACCAAGTGCCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCCCCCCTTCTCTTCTCCCTTGA CTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACAGCAAGAGAGAAAAGG[A/G]CCCCAGA AATCACAGGTGGGACGTCGGCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAACT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGTG[C/T]CTGGGAGAGAAGGAAGATG TTCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C	TTTACTATTTCAATGGATACAGAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCCTACATTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACCTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCACTATTATTATTATTATTTATTTTTTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGGC[A/G]CAATCTCGGCTCACTGCAAGCT CTGCTCTCTGGTTTCATGCCATTCTCTGCTCAGCTCCCGAGTAGCTGGGAATACAGGCCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	99 A G	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGTGTCTCTGCTC[A/G]GAGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T	TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTGTGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGAGGACCTGGCTTACGCTGCTCAGCCCTGCTGCTGCT[A/ T]CCAGATCACTGTCTCTGCAATGGCCCTGTGGATGGGCTCTGCCCTGCTGGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T ...			GGCCTCCTCTCTCCAATTCTGTCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTTCAATTAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTGTTGAAT
EST65258 8	80 A G ...			TGCCCATACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCC/G/GCCCTCAAATGACAGCCATGGCCGCCGGTCTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGAGCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGTTAGGTGCGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ...			ATGCAGGATGAAGGTGGACAGGGAGGAT/GAGGGCCAACTGTCTATCCAGGCGCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGG
EST62782 149 G T ...				ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTACCTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTC/G/TAAAGTCCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ...			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ...			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTAAAGTAACTGCTAAGTTTTTCCATTAAACCACCTATTACTTCTAIA/ G/GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ...			ACCTCACCCCTCCCTTAGCCGTGGGAGGAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
ESTD- KRT8a	21 C T ...			ACCCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCA/C/TGTCAACATTGACACA
EST75099 6	82 C T ...			CACCTTGCTGTCTAGATCTCCTCAGTGGCCGCTCTACTGGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTGGCCGCTTTGAGGTGG

ESTD- LF79	142 A G	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTAACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAATTTCCAATATGTAGTGCTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAG/GGGAGGGCTTCCTTACCACCCAGA
EST35879 9	142 A C	GAGATCGGTGTGTGAGTTATTAGGCATGTTACCTGTGATTCTCCCAATCTTGTGCGTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG[A/C]ACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G	TACACACTTTCTTACCCATTCACTGAAACGACTC/GIGCAAACTGGAGCCTTGAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T	TGTCAGTGTCCCTAGGGCACTCACCACCTCCAGCTTCTCAGCTCTGGCCTGTCTGCTGCTGCA AGGTTTGTCTTAATCTCAATCAATGCTCTTCATCTTTAG[C/T]AGCTGTGGGTTTGTGTTG TTCTCTGTTTGTCTAGTATCTGACTACTTTTAAATAAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MCC	45 C T	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGCTCCCTAGC[C/T]GAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTTGGTCTAAGTGTGATTACC[C/T]GGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	25 A G	ATTATCCAGATGAATTTACAAAAC[TAG]TACCAGATCCACAGACTGATATGGCTGGT
ESTD- NFKB1	107 A G	AAATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAAAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCT[A/G]GCCAAAAACGCTTATTGTGT AGGATCAGCCCTCATTTTGTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATTCT GAGAAAACTTCTTTAAACCTCACCTTTGTGGGGTTTGTGGAGAAGGTTATCA
ESTD- NPPA	45 A G	TGTCCTTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTT[C/A]GCTACTGCAAGAGAACACA GACAT
ESTD- NRAS	202 C T	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACITTTTGTGTTGTGATTATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTTG C/TATCCCTGTGGTTTAAATAAAAT
ESTD-PAI1	100 A G	GCCACCAACACCCACCCAGCACACCTCCAACTCAGCCAGACAAGGTTGTGACACAAGAGAGCCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG[A/G]GTGAGCCGTGTATCATCGGAGGCGCCGGG CACATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	CTCTCAGGAACCAACAGTCTTCTTACCAACACGACTTATTGCTGTCCGAGAGGTACAACCCGTAGA ACTTCTTCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTAGTGTTTCTTCACTTTCTGTTCTAGAACGTTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCATGCCC
ESTD- Per/RDS	74 A G	ACCTACAGACGTCGCTGGATGGTGTCTCAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGA/G/GAGCGTGGCGGAGACCTGGAAGGCCT
EST68308	29 C T	GGAAGAGATTAAAGAGCTTGATTGGA/C/TAATTCGGTCTTTGAGTGTGGAAGAGTTCATGTC TCTGCCTGAGTTACAACAGATCCTTTAGTACAGCGAGTAATAGATATATCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGTAAGAAAGTAGTATTTTTTA
EST54045	39 A G	GGAATATTAATAATTTTAAATACCTCCATTTTCTT/GTTCCTTTTGTGAAGATGATACCTGC AAAGACATGGCTAAAGTTATGATTTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGAAA TCTGTTAAGTAAGTACTGTTTGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
ESTD- PXMP1	88 A G	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAA/A/G/GAGCGAGCTGTGGTGAAGGTTTCTCAAGGCTCATAC AGATTCTGAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAAGTCTTATGAAATTAATCTT
ESTD-RDS	127 A	CCCAGGAATCTGAGAGCGAGCGAGGGCTGGCTGTGGAAGAAGCGTCCCGGAGACCTGGAAGG CCTTCTGTAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGGAAGCCGCGCAGACGCGAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- s14544	94 G T	TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTG/GT/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	45 A C	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/A/C/JTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C T	AGGAGAAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT/C/JTGGCTCAG GATGCCGGAAAATGAC
EST76136	39 C T	TGAAGCTTCTGCCAGCTTGCAATTGTTCTAGGAGAACCC/C/JTGGTCAATACCTTTATCTATAGCCTT CCCTAGGTCCT
ESTD- SPTB	176 C T	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACTTCTTGGCCCGGAGAAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACAC/C/JTCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCCAAGCCAGTTCTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C	---	---	AAATGGTCAGGACCCGTGATCCAAAGAAGTGGTACCAATTTTCATCAGGGCCATCAGTTCAATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATCTTAAATGACTTGTGGACAGGATCA ATTTCCTCTACCTAGAACGTTTGTTCACAACTTTCTTCAGATGGATGGGATTAATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THPB	125 A C	---	---	TGGGCTTTCTCCGGCAGGGTAGACTTCCTACTGGCTGTTGATTTCCAAAGAGAAAGAGTCCCAAG CACAGAAACAGAAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACACAGGATC[A/C]CTTCAT CCACACTGGATTGGCCAAACAAGTCTGAGTGCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTTCTGTTCCACCGCAAGAAGAGTCTATGC CAAGCAGAAAAGCTGGTGCTTCATGGGCAAAATCAATGCTCTCCAGATTTCA[G/T]ATCCCCAA GCAGTGCATCCATTGACACATAAATATGCATCCAGACAAAGAGGTCAATAAATTGATGTCGTATAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 GT	---	---	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACITTTATTACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACITTTATTACCTTCTTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C	---	---	TTCCAAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 CT	---	---	TTCCAAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCAAGAGACAGGAAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 CT	---	---	TTCCAAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	TTCCAAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCAAGAGACAGGAAACACCA GTGACTCTGAGATGTCAAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGG ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACAGTGTCGCGGGATGGCCGCGGAGTTC TGGTTGCGGCCACGGCTGTGCCCTGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGAGGGGGGGTGCCTGAGATGTAGATGGGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGCTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTTTATTCCTGAAGTCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGTTGAACAACAAGAGAAAACCACTGCAGAGTACCAGC/GTGTTGGTGGAA AGGAGTGCACAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNF α b	152 A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGCATGAGGACGGGTTAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAG/GGAATCGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTTGATGATG CTGTGTGTCCTCAACTTCCAAATCCCCGCCCGCGGATGG
ESTD- TNF α a	88 A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGTTTTGAGGGGCATGAGGACGGGTTAGCCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCTCAGAAATCGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTTGATGCTT GTGTGTCCCAACTTCCAAATCCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGGAGTACGGGCTGCAGGCATACACTAG/GAAGTGAAAACCTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTTGCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTTAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAG/GGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGCCCCCATGGGGGACGTGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG/ATCTCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGGAGCAGCAGGAGGATGCTG GGCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCAG/TTAAAAACATTTCTATGAGCCAGGAGAGATACGTATTCTCTGAAGCCGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ...	---	AGACCTCAGTTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC/C/TJAGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	108 C G ...	---	CGGTCTTCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCAGATGCATCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTTAC/C/GJGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ...	---	ACCTGGTGTGCTGCTGGGTGAACCTGGTCTCTTGCCATTGCGGCCCTCTCTGGGCCCGCTGG TCCTCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTCTCTTAC/C/GJGTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGTTCCCGAGGTGCGGATGTTCAACCGGACACAAAGGAGAGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ...	---	AGTGACTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACTCCACTGCAAGAACAGCATTCATACATGATGAGGAGACTGG/C/A/CJAACTGAAAA AGGCTGTCAATCTACAGGGCTCTAATGATGTTGAATGTTGCTGAGGGCAACAGAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G ...	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGTAGACAACA GTGGTACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTTTC/C/GJGGGTTCGAAGGTGAAAA GGTGAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAACTACTGCCT TTGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ...	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACA/C/JTGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ...	---	GCCGAATGCCCGGAGTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAC TGGAGGCCCGGCAT/C/GJGTGCTCATGCTGTAAATCCAGCATTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ...	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAATATCTTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCGATGGGTGAGAACTGTTCTGTCCACATGGAGGATACTATACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ...	---	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTTGCTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCACCACTGCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T	TTACATTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGTCTTGGCTGCCTGTGCTTGTGGGATATTTGAAAGAGATC/TTTGCCAGTCCAAATGCTCCTAGA GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCTGTA
ESTD-RVRI	109 A G	CTTCGTACGGGAGGTACAGTCCTCGGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCCTC CTGCTGACAGTGTGATGACCGAGCGAGACTTGTCTACTATGAG/GGGGAGCTGTGTGCACTCATGCC CGTCCCTCTGGAGGCTGGAGGCTGAGGACATGAGTGGAGTGGAGCCACTGCGCTGGGGCCAGCC ACTCGAGTCGGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCGAGGATGTG CG/GJCGTGTGCTGGAGTAGCCCGGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCAATGTGTCTTACCGAGGCTGCAA
ESTD-F2	100 C	GATAAGTACACTGAGGCCCGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGAACTGGGGGATCTAGGGGATGGTGAGGAATGGCCCC AGCCAGTCCGGCCGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGC TGGATGAG
EST44438	62 C T	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATTGGGACCTCAAGCTCGACTTCAAGGA/C/TG TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
ESTD-PBDA	103 A G	CCTTCTCATGCCAGATGGAATTCAGTCCCTTACAGGATCTGCCTAACCTGTGCAGAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCAA/GJTCCTACCCGCGAGCTTGCTGCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
EST12839	122 A G	TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCTCTTTGCT CCTAACATCTATGTAAGTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJTCAGTGCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAG
ESTD-CTLA-4	48 A G	ATGGCTTGCTTGGATTTCAGCGGCACAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG CACTCTCCTGTTTTTCTCTCTTCATCCCTGTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAAAGCCAC
ESTD-ACE	96 C T	GATCAAGGAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGTCTCCCTGCTGGGGGGCCAAACCCCGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCGGCTCTCCACTCTGAACTGTGCACAAAATCGGCCCTGC
EST54419	88 A G	CTTCTGCCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGATTTGGGTTTAGCGTGGTTCGTATGTTGTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACCTGGATTGGGAGATTCAATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAATAGCCTT/GJTTCGTAGCCATAATTAATGGTTTGTGCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGGCAGCTCTCCAATCCATCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGGCGCCCTAGCCGGGCCCTGCTGGCGCTGGCGTGGGTGGCCACOC GTGGAGGCAACCTGCTGGTCACTGGGCCATGCC/CJTGAGACTCCGAGACTCCAGACCATGACCAA CGTTCGTGACTTCGCTGGCCGAGCCGACCTGTGTGATGGACTCTGGTGGTCCGCCCGCGGCGCA CCTGGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTGGTTC/GJAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTTCTCTCCAATCCATCTTCAAAG GCTGCCACTGTGATCTCCCAAAGGTGATTCTGTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCTTTCT/GJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCCTTTCT/GJAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTAATTATTAAGTCTATTCTGAAATATTAT TTTTTACA/GJITACCCCTTTGATTATTTTGAATTCATTTGTAAAGAGAGATTACAATATCAGTAACGC TGTTCAATGATAGTGCTATCACAATGTCTAAATACATTTTGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATGCTTGATGAGCCTCT CAA/CJTCTTAAGTCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACITTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCCTGTCTTCCCGAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTACATTTAGAC AGG/CJGJAGCAGAAGCAGCAAGGAGGAAAGGAAGT

WI-2625	98 G A ...	---	---	GGG CAG T C C T G G C T G A G T A G A C A G C A C T G A A G G A T G A G A G A G A A A C A G G C A G A A G C A C T G T G G T A G T A A C A A G G C T T A T T A G G A [G/A] C A A T T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T T A T C T G T G G T G A A T T C A G T T A T C C A C T T G C A G G A G G A A A G C C A G C C A G C A A A G
WI-2924	54 G A T A G G	G C C T A A G T G T A A T C A C A G G G	T G A C C T T C C T A G T C T T C T C T T A	T C T G T T G T C A T A T T T C C C T C T T T G A C T C T G A C C T T C C T A G T C T T C T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T A G G G C C T A C C T G G A T T A T T A G A A C A A T C
WI-2939	72 G T G T G C C T T T	C T T G T G A G G G A A G G T C T T G	G G C T T G T C T C A G T G C C T T T	C C A T T G T G A G G T G G G T C A C T T G C A T T C C C T G C A C T C A C A A A G T G G C T T G T C A G T G C C T T [G/T] C A A G A C C T T C C C T C A C A A G A A T G T C T T C C A T G C T C C G T G T C T T T G A A A A T T C G A C T T T A T C C T G A A A A C T C A G C T G C A G T G T T A T C T C G G T A T A A G C C A C T C C T G
WI-3203	99 G A A G A C G A G	T C A A G T A T T G C C T T G T G T G G	G G T T A T G C C G C A G A C G A G	C T T G C T A C C A T T T C A G A C A T A C A C C C T C A G T G A A T G C C G T A A C C C C A T T A T A A A C A T C T T G C C A T C G A A G G G T T A T G C C G C A G A C G A G [G/A] C C A C A A G G C A A T A C T T G A A G T G A C T T G G A G A A T A A G A T T T G G A T G G A T G A A A G C A G A G A G A T G C T A A A A G T G A
WI-3473	101 A G C C C T A G G G A	C C T G A T G T C A C C A A C A T T T T C T	A A G C A T T T T A G C C C T A G G G A	G G A A A A G A A A C C T G A A G G A T G A G T A G A A T T A A T T G G A G A T A G T T G G T A G G C C C T G T T T G G A G A T T G C A G A G A A G A A G C A T T T A G C C C T A G G G A [G/T] A G A A A A T G T T G T G A C A T C A G G G C T A C A C A C T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G T C T T G G C T C C C
WI-1796b	29 A G ...	---	---	A C A C A C T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G T C T T G G C T C C C
WI-1796	29 A G ...	---	---	A G T C G T C C A T C T T C A G G G T C T A A C T C T G G A T C G G C C T G C A G A T G G A A A A G A A G A T G G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C C T C T G A A A A A T A T C T C C C A T G T C C C T G T C T A A T A T A C A T T T T C C
WI-4360	93 C T A A A T A A	T T T	G T A G T C A C A T T A G G T A T T T C C	G C T G A C T T T G T G C A G A G C C A G G G A C A A T T C A G C T G C C G G A T T T A A T A G A T T C T G C A G C A C T G C A A C A G G A A C C A A A A T C A G T C [C/T] G G G T A A C T G A G A G T G G T T T T C A C A C C C A A A
WI-1959b	87 C T ...	---	---	G T T G T G C C T G T A G C A G A C A C A G A G G C A [A/G] A G A G G A A A A G C C T T T T G T C C A G G G C T T A C A C T G A A T C C C C T C A A C A A T G C A A G A T G A G C T A A T G G T C T T A G A G G T A T A A T C T A A G T G T G A G A A A A C A A A G G T A G G G T T T G
WI-1973b	28 A G ...	---	---	C T T G A G T A T G C G T G G A T T T G G T A T A C A G A A A T G G G A G A G C T G G A A C T A A T C C C C C A T A T A C C A A G G G A C A A A T T G T A T C T G T T T C A C A A T T A C A G T A G G A C A T T A T G T C C A T G A C A A T G G T A A T T T T A A [C/T] G A C A G T T T T A A T T G A G T G A A A T T A C C A T A A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T A C T A G G T G C C T A T A A A T A G C
WI-1980b	140 C T ...	---	---	

WI-2015b	190 A G	TGTCAGATAGTCGCTCTACCTAGGTGCAGTAGGATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAACTCTACATGGTGTCTTTTCCAACTA/GJCATATACCTT CTAATACCATAGAG
WI-754b	49 C T	GAAGGCACAGGGAGAGATGGCTGTCTATCTACAGCCAGGGAGAGAGAGC/TTACATTTATTGGTAA TCCTATAAAGTGCAATCTTTAAATTTTGTATTACTTTAGA
WI-754	22 T C	GAAGGCACAGGGAGAGATGGCTGTCTATCTACAGCCAGGGAGAGAGAGCCACATTTATTGGTAA TCCTATAAAGTGCAATCTTTAAATTTTGTATTACTTTAGA
WIR-1b	56 A G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGGTGATGCCCTCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T	TAAATTTAAATGGGGCCAATAACACAGTACTTATCTACAGCATTTCTCTAAAGGCTAAATAAGAA GA/ATGTATCTAAAGTTATTAGCTCAGAGCCCTCACACATCTCAGTGACTGATAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T	GAGCCTTTCTAAATTAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C	CGGGACAGAGACAGAGAGAGAGAGTTCTGCAAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C	CGGGACAGAGACAGAGAGAGAGTTCTGCAAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C	CGGGACAGAGACAGAGAGAGAGTTCTGCAAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGATTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGATTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCGTGTGGTCCCACCTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGGTTTACGTCCAG
WIR-6	63 A	C	---	TAACCTGAAACITTTGCTCTCCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTGGGGCAG
WIR-7	12 C	T	---	TTGCTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C	T	---	GGCGTCTATGACTATCCTGGTCATTGATTTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56 C	G	---	AAACAGAAAAATAGAGGTTATAAGGATGGAAGTAAAGTTGTGAGAGAGGATGA[C/G]CTGAAG AAAGAACTACTCTCTTTTGACCAATAATAACAATTGGGAACACTGGAAACCATGGCTTGATTACT GACAAAC
WI-7069	93 G	A	---	TGTCCTTGCTTATGCCTCCTCTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTTCCCTTTTATCTGTGAGCAGCCAGCTGTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCC CCACATACCAACTTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CCTATATTTC AGTTTGGAAA TTGATTGCTG CTTGCAAT CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]ATTTCGAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAATTAATGAAAAACATCCCT

WI-18517	87 C T	CAGGAATCAG CAGCCTGA	TGTTGGACAA GTGCAACA	TTAAAAATAAATACTAGGGCTACCCCTCAACACCCCCCTCCATTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TGTTGCACCTTGTCACCAACACAACTGACTGC
WI-18868	76 C T	GGGAAAAAC TAGGCAAAA	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAAACCTTTATTTTCAACCTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/JAGCAAAAAGTGCAGTTTAAATTTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75 T C	GCTGTCACTCT AGCATCTGGA A	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGGAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/C/JGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99 A C	GGGTTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACCAACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCAGGGGTAC/C/JCCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29 A G	TGTGGCAACCTTGTTTTAATTGCAAC/C/JIACCTAATTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121 T C	GTCGTGGGTG G3GG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTATTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCAAGTGCTGGGGTGGGGGTGCAGAG/C/JGTGCTCCTCTTC AGTGGTATTGGGAC
WI-18533b	91 T C	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTCTTCTTTATTT TATATTTTCAATTTTCATCCTAAT/C/JTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
WI-18533a	59 T G	GGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTCTTCTTTGCTTTA TTTTATATTTTCAATTTTCATCCTAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83 A C	TCATCTGATAC CTTGTTGAGAT TTC	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTGAGATTTC/C/JAAATAGTTGTAGCCTTATCCTGGTTTTACAGATGTGAAACTTT
D49493	159 A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGGTGACGCTGCAGACACAGACAGACAGCTCATGGGCAACATCACTGGGGCCCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGTCTTTCTTCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT/C/JGCCCTGGCCTGAAAGTGCCCCATCATTCATACCCACTGTT CT
EST10030 7	98 T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/JTCATCCATACCACCCTGCTGATTG
EST10052 2	24 G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/C/JA/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTGCATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ...				CTTGGTAAATCACAGTTCTGTATTATACAAAAACTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAGAAAGATCCC
EST11048 0	61 T G TAATCT	CTCTCAAGTAG ATAAGAGGCA	GCTAAATTTTC AGAAAGAATT TTGTTT		CATGTGTCATCCCATGATTGAAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/JAA ACAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACAGAGAGGAGGCAC
EST11260 8	101 G T ...				TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ...				TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCAAGTGTGTTTCTTTGGACGAAGAAATCCT TCTGTGGATTACGCTTTACCGCTTTCTCTCATCTGCTGGTG[C/T]TTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G TGGAGCCCT	CCAACCTACTT TGGAGCCCT	TCCAGCTTTCT CTAAAACTCC T		GAATTCGGGTATTAATAGCGGGTCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[A/G]AGGAGTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGGA
EST11772 6	74 A G ...				CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[A/G]GACTATTTCACTTCTGACTATAAGTGAATAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ...				CTTGTCATTTATTTGTGCATGTTGTTCTTAAAGGCTGTGAAAGATAAAGTGGAAATGTTGGAAAC ACATAGATCCAG[A/G]ATTAAAGGGGCTGGAAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC		AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAGCCCTCCACAGAACTTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCTTGGAT		GCCTAGTAATTCAAAAGGAACATGTTTGATATAAACAACACTCAGTACAAAGTCTGT[A/G]ATCCAGG AAGTGACAGCCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ...				GTGGAAAATTTTTTATCTGTACGTCTTTCC[T/C]ATTATATTTATCTTGTCTTGTATTTTCAAGCAACC CACCCGATTTGCAGGCAGTGTCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT
EST12492 1b	95 A G ...				CCCCTAGCAATGACTGGAGTTGTGTCCAAATACCAAGTTACATACTGTGCCAAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ...				ATCTTGAGGTTTCTGGCCTGTCAG[A/G]AAGTGACATCTTTTACTACCAGGTCAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTAAAGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAACCAAAGTGGAGGCAAGTCCACAGGTACACACTGTGTCAC[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAATGCTCAGGGGGAATGACCAATTTTAAGGGCCATGTG GTCGTGAGGCGTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATAGAAATGTCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTACAAA CAGGTGTTTATATCCCAAATGACAGTGTGGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCATTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGG[C/A] /GTTGAGAATACAATTTGAAGAAGAGTCACTGCCTGCCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGATGGGAATCCATGTGCTTGGTACTCCATCAGGTCATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCAIT/AJCAACAGCCAGTTATTTACCAGAAATTTGTTGCGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTGTTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAAAATTCAGAAAAATCATCTATAGTTGA GTGTAAACCTCCCTAAATCAGTCTTTAGGGCCACAC[C/T]GGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAACCT
EST13117 6	68 A G ---			TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC[A] /GTAATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCCTCATAGCTGTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAATAGTCT GGCCATTT/GIGACTAACAGTTCTACAAATTCACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCGAGGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT G	AACCAGATTT TGCAGGCT	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CCTTTCTTTGGATACCTTAGTAGTTAACTCTCTTTTGCAAAACCCTCTTGATATAACCA

EST13278 2a	51 A G G	CATTACCGAA CAATATTTAG GTGGTGAGAA	CATATCTTGG GTGGTGAGAA	TTCCGAGAACGTTTACAAGCTCCAAACCTTTACCCGAACAATATTTTAGGAGAG/ATTTTGAATAT TTCTGTAGTTCTACCAACCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGT	GCTCAGTAGATGAGCATTGACCAATATTTAGATAATACCTGTTGGGAAAGTGCTGAATTAAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAAG/ATTAACCTTCTCTCAAATTTTCCATCTCCCATCAGA
EST13290 9	39 A G CTT	CAATTTTGA AGTTGGGTT	AAATCAGTTCA TGGAATTTCA G	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT/AG/CTGAAATTTCCATGAAGTGAATTTT TTTTCTGTGCTTAACCTTCACTTAAGACCTAAAGACAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTGG
EST13518 2	45 C G	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTGAGCATTTA/C/GIACTTTAAAAATTAACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	68 A G	CAGGTTGGTGATTCTCAACTAGGAGCTATTTGCCCCCATCCCCACCGGAGTGCTGGAGAC/AV GIGTTTGTATTGTCACAACTGCGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AAT/CJGCACACAAGGAATAAGGGAGAAGGAGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACACAATTTTATAGCAGGTAAACCAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAAA/C/GJTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G	CCTCAACCATCTGTAAACCCGAGCCCA/GI/CAGTGACCGGAGCTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G	CAATGGTGTCATGTGAACATAT/AGJACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAGTCACTCTGCTAAATGACCGAACACAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATAATTTT AAAAGA	AATATCAATGCATCTTGTGGCATGCTAGACAGAGGCATTAT/CJTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTCCCTTCACACTCATTTTAAATGT
EST14812 2	50 A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTAG TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTTCAAGTCAGCTTCTACATTTCTGAATA/AGIAGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGAGTTTGCCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCAACC ATACTGGTT	CGGGAAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTCTCCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTAAATAAATCTGCGGTCATCACCCACCATACTGCTT/ATTTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A	TTTAAACCCAAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTATCATATAATCATATAGCCAAAGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAGAAGACAA AGACAACAGA		GGAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAAAGACGTGAAGAAGACAAAGACACAGAGGA[G/C]AGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGTATGATGATGTAGTA
WI-16739	57 G A	GGTTTGGCCAT CACAAAGC		GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T	GGTGGGAGTCT CACTGTAAGG		CTTCTATCTTT CTGTTCTCTCA TC	CTTCTTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGATTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA		CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAAAACTTAGAGGTTGCCTCTTTTGTGTGCATTTTCTCTGAGATGTCTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C	CAGGACTTAAGTCAATTTGCCTGGAAGACTTTAACTAAAGGTGAGGCAACATAGGA[T/C]TGTGA CAGCACCACTCGGACCAAGGAGTGTCTGAAATCGTCACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C	GGTTTGAAGACGAGCTTATCTCCACCTGCCACTGGGATTCATTTTGAGAGCTGTTTGTGACGCC TTTTCCAGAAAAGGCCGCT[C/G]GGGTTTTCTGAACCTCTATGGGCATTTTGAAT
EST16089 9	96 C T	CGTCTGAAGTTTTCTTTATCACAAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTCACATTCCCA GGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGTATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTCTCTCCAGGA[A/G]TTGGCCCCGAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C	ATGGTATAACAAAATCAGTTCAGGTTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CAGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G	ATGGTATAACAAAATCAGTTCAGGTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCTTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ...			AGCCAAATCAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATTATC/TJAATGAACGT AAATAATCAAGGCAATTTTGATCTAAAGCATTTTGCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGATAGGA
EST16182 6	54 G A ...			CATTGGTTGGTAGGGAAAGATAGTAGTGCAAAATAAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTCCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGCAGAAAGTAGTA
EST16183 2b	59 A G ...			GCAGGTAACTGTGGTTACAAACGTATTGTTCTTTTATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTCTCGGCCCTTCTCGTTTCATATTTTATGTCACTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ...			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTGCAATTT CCCCAGAGGAAAGTCAGCATCATAAACACATGGGTACATGCTCAGGCACATGGTGTC
EST16229 2c	52 T C ...			TGTGAACCTCGAATTCGCTTGTCCTGTCCTGAGTCACAGTTTCA/TTC/TGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAAGTACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ...			TGTGAACCTCGAATTCGCTTGTCCTGTCCTGAGTCACAGTTTCA/TTC/TGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAAGTACTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTTGGCTGGAACCTGGTCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTCAATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ...			GCCACTCTCTGTGGCTTGCTCTGTCCAGCTGCTGCCAGTGCACACAG[A/T]GGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCTGTGCTGCCACTCTCTTCTTCTTCCGCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ...			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAAGGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGCTG	CAGCTTCTGAC	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTT/C/GTTCTTATGAAGAAGTC AGAAGCTGATAAAGCTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ...			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTACATAAAA AATGGCTTCCAAACCATTAAAAATGAACTT/C/GGAAATAGAGCATAAACGGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCTCCAAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA

-201-

WI-16879	79 C T	GATACAGGC ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCACTATAGGACTCTAGTTCTAGAAAGCCCTGGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACTCTTAGGTGGGAGAGACAAATTTCTCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTCTGACAGGCGATTACCTGACATGTGTCACTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTCTGAGTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTGGCCTGT GTGTTCA	GTCATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTCCTCCCAACATCAGAACATAAGTTCCATGAAAAACAGGAACCTTGGCCTGTG TTGTTCACTGCCACTGCCCTAGAAAGATATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAAGTAAAGATGGCG CTAGAAAGTATCTGTTATAGAAACGATACCTTCATTTGGCCTGAACCGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCACGCTGATGCCACTTCTGTATCAGGAACCTTAACGCTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACJCCA CGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAAATA GGCTGGAG	GOCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAATAGGCCTGGAGCJGJACAGG ATTTGGCTGAGGCTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAG TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATACTTAACTTGGTCCAACCTATT AGTATAACTAATATGAGTTTATCTGATAACTTGAATGCCATTAAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAAATAGTATTTTJACGGCTGG AAATCAACATGCGCTCTCTCTGTGTGAAGTTGTACGATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60 T G	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGAGTACACTGTGCGCCCTCATCTGAGATJTGJTG TAGGACTGTAAGGGAATGTGTTGGGGGTTAGGAA
WI-16992a	46 G A TC	AAGCACCAG AAGTACACTG	CACATTCCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCCAGAGAGTACACTGTGAGJCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTGTTGGGGGTTAGGAA

WI-17010	23 T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T T C A A C A G G A A A G C C A T G [T/C] A T G A C A T T C A A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST 17127			G T T T T G A A T G T	T G T T T A A T G C A G A C A A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T A C C C T A G A C A C C T A G A
9b	74 C T	C A C T C G G C A C	C A	G G T T C C A C G
		A A T T C T C T T A T	G G G A G G C A G G	A T T C C G T C T C A A A C A G C A T C C C A G G C G G G C A T C C C C C A C G A T T T T A T A A T A C A C T C G G C A C A G A
WI-17040	94 T C A	C A T C T C A A G C C	G G T G	C A G A G [T/C] T T G G G A G C C A T G G G C A C C C C T G C C C T C C C C A G G C T T C C T A A G T A A C A A C T
			G	C A C G C G T T C A T T A A A T T T G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C
				G A G A A T T C T C T T A T C A T C T C A A G C C A G [T/C] A T C A C T G A A T A A G C C A T A G T C C C A G T C T C G T T T T C C
				A A A T C T T T C T C A T A T T G T
		G C C A A G G G A T		T T G T T T G T T T T G T T T T C T C C T G C C A A G G G A T T A A C G T A T A G G [G/T] C T T A A C A A G G G G A T C
WI-17044	47 G T G	T A A C G T A T A G	G G G G A T C C C C T	C C C C A C T T A T A G C T G A C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A A T G C A G G G A A T C G A A T
			T G T T T A A G A	C A A A A G A A A A G C A A G T G
		T G G A C T T G T C A		G C A T G T T T G G A G C A G A T C C C A T G G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C [T/A] G
WI-17021	62 T A A C T C	G C C T A T A A C T	T G T A G A G T T A G	C A G C T G C C A C T A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A C A C A T G C C A A A G T G C C T G G
			T G C C A G C T G C	G A G G T G C C A A T A A A A T C A A
		C C A G A A A G G A		
WI-17065	90 T C T T	A A A G C A T A A A	C C C A A G A G A C	T G T A A A A A T G T A G A C A T G G G G A A A A A C A T T C G T A A T C A A C A T G T G C T G T T T T C T A C T T C C G G T A
			A A T G A A A T C C T	C C A G A A A G G A A A A G C A T A A A C T T T C A G G A T T C A T T G T C T C T T G G G T
		T G T A C A G C C A	G A G A T G T T G A A	
WI-17068	32 A C T	A C A T C A C T G T T	A A T G T T C T G G A	T T C A T A A G G T T G T A C A G C C A A C A T C A C T G T T T [A/C] A T T C C A G A A C A T T T T C A A C A T C T C A A A A A G A
			A	A A C T C T G C A C C C A T T A G C A G T C A T T C C C T G T A G C T T C C C T C A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86 T G ---		---	T G C T G A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T C A A C T G T T C C A A G C A T
WI-17104b	108 T C ---		---	A A C C T C C T A C A C A G G C C T T [G] C T A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
				C A G A T G A G A A C T C A T G C T G G C T C A T C T G A A G C T T C C T G A T G C T T T G C G A G C T T T C C C A T T C A T T C C A
				A A T C A G A A G C A G T C A G T G G C C C C G T G G T T C C A G A C G G C T T [C] T C T C T T T G T T A A G A A A T T A
WI-17114a	37 T C	T T C C A T C A A G	T T G T A T T A A	A G C G T C C A A C A G A T G T T T C C A T C A A G G A C T T T G T T T T [C] G T C T C T T C A C T C T G C T A T T T A T A A T A C
		G A C T T T G T T T	A A G A G A C	A A G C T A C C T C C C A A G G C C A G A T G C T A A G T G C T A A A A A G A A G A G A C T G C A G C C A A T C A G A G T T A C A T
		G A T G A A A T T C	T T C T C A G A A T C	G G G A
WI-17150	76 T G C T C T T	A G A T A G T C T T C	C T G G A A G A T A T	C G T G G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C C C A C T G A A C A G G A T G A A A T T C A G A T A G T C
			G	T T C C T C T T T [G] C A T A T C T T C C A G G A T T C T G A A A G G C C C T C C T T T G T C T G C T C T A A T T T
		C A T T T C T T T G T		G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A C A A T A A C G T T [A/G] A A G G C A A A A G C A A G A A T T C T G
		A A A A T A A C A A	C A G A A T C T T G C	T A A C C A C A A T T G A A A A G G G G C A C A G G G G C A G A G G G A A A G G G C C A G A T T T T C A A C G G T T
WI-17163	43 A G T A A C G T T		T T T T G C C T T	C C T C C A C A T C T G C A G A C A A A

WI-17178	127 T	C	GGACTCCCTCA	CCCTCAATTTT	AGCAAATGTCCTCCCAATTCATTAGCTATGAGGTTATCAGTTTCATTTCAGAGCGAATTACTGG GGCAGGGGTTTAATATCTGATGGTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C	G	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACCTTCCCAAGTCTCGTCGCACAG GCTTCAACAATTAC/C/JAACATCTTGCCCAATTTGTTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T	C	TGCA	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCCTGCACCTTC/C/CCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCAACATCTTGCCCAATTTGTTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17158	54 G	C	TCCCA	CAAGAAATAT ATATTTGATTG	TGAGGTAGCAGGGCATCTTAAGAAATGTTCTCTAACTTTAGATATCTCCCATTC/C/JTTCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATTCCTG
WI-17149b	79 T	C	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCATTC/C/JGTGATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17149a	48 C	G	AGGAGGAACA	CCACGCACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTCATGCACGTGCGTG GAAACCCAAATTGTCATGTGTATGAACACTACAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17197	67 G	A	CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAAGTAGCTGGGCTAC/C /A/JGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTAATAGAATAATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTCTCCCTGCTGCTAGTTTTC/JTAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
WI-17198	38 A	C	CCTAGTTT	TCCATTTGTCC ACTGAGAAAT	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCCTGCTGCAGTGGCTGG GATAAGACACAACCTGCCACCAGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
EST18753 8	27 C	T	GGTCTCAT	GGATCGCATGA GCTGA	TTATTTTAAACATAACCAGATGCACCTTGGTTTTTACATTTCTGTTGCCATTCAAGTCTCAAAGT AAACAC/C/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT
WI-17108b	74 C	T	CA	CC	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/J/GJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCCATCAACATTCATCATCCATCTCCGTT
EST19067 2b	41 A	G	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/J/GJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCCATCAACATTCATCATCCATCTCCGTT
EST19067 2a	40 A	C	TTC	CCCA	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/J/GJTGCGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCCATCAACATTCATCATCCATCTCCGTT
EST19125 8	28 A	G	CTGTTTCTCAGAGATGACACTGCCAACA/J/GJTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTTACAGTAGTGTGTTTTTCTCTCGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTTCAATCAGTCTCTGAAATCAGGGATTGAGGTTTTTA AGGATAACTTGGTAGAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTTGTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCCTCAGAACTTCTCAGCCTAGG]GTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128 G A GTG	TTCATATGGCC ATTTTAATAA	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGAGTTTCTAGTGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATAGCCATTTTAATAAGTG]G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATTCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTCTTTT/C]GTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78 T C TATCCTGCCA	AATTATTCTGC TATCCTGCCA	ACCATGAAGG ATGGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCCTGCCATT/C]ACCCGCATCCTTCATGGTAGAGTATCACAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C ---		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTACTCTA]T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22311 9b	54 A G ---		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCC]AG]CCACTGTAAA CAGTAGCATTCAATGGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22311 9a	41 T C GAGTTATAA	GGATTAGATC ATCTTTTATT	TTGAATGCTAC TGTTACAGTG	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATAT/C]ACATAAAAAATCCACCACCTGTAAA CAGTAGCATTCAATGGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATTCAG
EST22319	19 A C ---		---	TCGAGGAGCTCTGAGGAGC]A/C]ACCAAGGGACGTGTGCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCCCTTTGAGATATGATGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCAAGGCTTTACC]A/G]TCTGTCAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G TTATCTGCACA	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAAATGACITTAATAAATACTATCCAGAAATGGATCCTTATCTG CACA]A/G]CCATTGAAGAAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCCC	TTGCGTGTAA TTTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTACCCCCA ATTTCATTACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCATTGTGTACTTATATCTGTACAAGGTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTAAATTTATTAATCTTTGCCTTTTATGGTTTTGACAGTTTGTGCTCTTTCT T
WI-17387	55 C G	CCTTTCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCCTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTGTGTCGAAATAGATGAAAAGAGAAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACTAGGCAATGTAACTCCAGAGGCAG[C/G]CTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTCTGCTCACTG
EST23733 9	31 T G T	GGCTGTAGTT TTGTTTTGTT	TGCACCTTTAA TCCATCAAT	AAAGCTGTAGTTTTGTTTTGTTTTCTCTT[G]TATTGATGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGCCTAGAGAAAGATATAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGC TGAAGATACCCACCTAA
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCTGTGTGCGGGGTGCTCATGTGCGTGTGTGAGTGAGACATTTTTACTGCGTCCC GTCCCGCAGCCCTA[G]TGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGCTTGGTTGGAA TACCATCAGCCTTC
WI-17519	55 T C A	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTAACGAAATCTCACTACTGCAAAATGCATTTGTTGCTAGCTAAATGAATGCA[T/C]JAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCITTGATACAGGTAAACCAGTTTGTAACTATTACAGAACTTCACTGTATCTTCAAGTTTTGATAT CAGCATCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCITTGATACAGGTAAACCAGTTTGTJA/CJACATTATTACAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA[C/T]TAGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATCAACATT ACTACCAGTT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT[C/G]ATAGAACCCAACTAGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAAGGCCTACT TCCTTGTGTAACACTCCCA/GIATATTGTCGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTC

WI-17623	46 T C	TGTGGTTTAAATTTCCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATTCATATATCTTTTGGAAGCATCTGCTCCAATCTTTGGCTGACITTTGGAGTTTTTTGGT
EST26419 1b	46 T C	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGC/A/AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGAGTAAATTCATGGTAAATGTCATGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	CAAGAAGTTTG GACTGCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGC/A/AACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAGTAAATTCATGGTAAATGTCATGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780	69 G C	TCAGCTTTAATTTAAGGGACATGTAATAAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCCTGTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G	TACTTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC/A/G/GAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGCATGACGGGAAGCAGAG
EST27152	101 C T	CAAAAGGATTTTATTTGTTCCCTAAAAAGTAAAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACATAAACATTTCAATCAATCTCTCTCTC/TCTC/TTCACATGGTGTACTCTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATT	GCTGGTGTGAT GCTACTGTAAT G	TTTTGCACTTTGCAACAATTAATAATTTATC/G/A/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTCAGTATTTCTGTACACATTTCTGTTAACAGAACCCCATACATT GGTAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG C	TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTTCTCCAGTCTTG/C/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100 A G	ATTTTATTAGCGGTACAAATCCAAAGGTGGTAAGGGTGAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAAAACAACATTTACATTCAAGGAC/A/G/GCTTCCAGACAAGCCCATGTAGAACCAGCAT GCCTTGGGACTGTGGAT
EST27828 4	58 G A AGAAGTCAATC	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAACCTTCTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCAAC/G/A/GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAAATTTCAATCTGTACACACAATC/G/A/AAATG GATAAGGCTCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/C/JAAAAGAATGATCAATCCTGTTCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACACCCGCGTGTGAAGGAGACTGCTGTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTGCAAT TATTTTATAC CA	CATTGGAGTAAAGGTGTTCTTCTTTAAATTAATGATGGTATAAAATAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACGAGACATGAGTTGTTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCTCTCC TGTC	TGGGTTGGCAG TGTC	AGAAATGGTCTAGTAATCGTTTCAGGATTTCGGTGATGGGCCCTCCCTGCTC/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAGTTACATCATACCAAGTGATACATACTG TTT/CACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGCTATTAC/GTTACATCATACCAAGTGATACATA CTGTTACATGATTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST28041 5b	53 G A	GGAACAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACATTAAAGCATCATTTGTCACCT[G/A]GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	CTTTAGAAGGACACACAGTCTGTTGGACTTAGGGCCTACCCTATCCAGCAGGTGCC[G/A]TTATTT TCACTTGGTTACGTCTGTAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT[C/T]ACAGAAGAATGAGACACTTACGCGATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	TATTGGTATGCTTAGGGAAGATTCTGATTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAACTTCTGTTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99 A G	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAAATATTC[G/A]GGATTAAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	CTTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCAACAATATAGGTAGC[G/A]ATAACCAGGTCCTACTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T A	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAACTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA[G/T]ACCC AGAGTTTCAATATAGGTAGCAGTAAACCAGGTCCTCATTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTG[G/A]GCCTGTTTCTTATACCCCAATATCATAGAAT GTTGTTGCTTCTATATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTCAAAA

EST31951 4	87 C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACCTCC	ACAGCCATTATTATGTTACTTGGTAATATCAGAGACTGAACACATTTTCTACTCTTTTAGCAATGACA TCGGGTTGTCAGCAACAAC/C/JGGAGGTGATTTTGGTGGGAAATCTTATCACAATTATTCT
EST31968 8b	95 T G	CGAATTTGCTCTCTATTGTTGATCTAGTAATCCTAAAGATTTGGGGGGGGGTTACTATAAGT GCATTTTATAATGGGGATTTCTGCTT/GJAACTGCCCACTGATTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75 T C T	GCGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTATTGTTGATCTAGTAATCCTAAAGATTTGGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103 C T	TCCATGGATGAACAGACGCTACCATGCCACATCCCACATCCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCCTCCAGACCTAGCTGGCTTTGTAGT/C/JGTTCCAGGCCCATTTGAAATAGCAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	AAGGCTTCCAAAGCATTCAAAGGCACCTGGGTGTTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/JVG JTCGTGATTAGGGAGCACCCCAAGCCAGTAACAATATGGTTCTTGCAG
WI-17800	29 C G GAGAACTCA	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/GJAGACTGGGATTAATTGTAGGAAATATTTACACAG TTCCACAAGTCAGAGAGCTAATCCCAACCCCTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AACTGTCAATTCCTAAAGTCTGGGATGACTTTCCT/GJATCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAAATCCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCATTCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAGCAAAAT/T/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A AGCAAATA	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATGT/T/JTTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
EST33301 4c	80 G A	GAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA/GJAACTGGATGCCAAAGAGTATGG
EST33301 4b	63 G A	GAAAAAAAGTCAAAATGTTCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT/GJ/A ATCAATGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44 G A CA	AGCGTGGTTT CAATACTAAA	CTGTATTATT GTTAAATATT GCATTGTT	CTATCCAAAGATATTATTGCAGCGTGGTTTCAATACTAAACA/GJ/AJGTAAACAATGCAANTATT TAACAATAAATACAGTGATTAAATAAGCCATGCCATATCCAGTTGATGTAATACTTTTGCAA

WI-17904	50	A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACAC[A/G]TACGGGAATTAC TATTAAACATAAGCGGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACACAAATGA
EST34149 5	69	A G A T	TGCCAAATAC TCAAGTGTGA GAT	AACACTAGCG AGAACAACTA ATAAAATC	GTITTTCTTTGAGTGACACAAGCTTGTTCAITTTTGAGAAAATGTGCCCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95	C A	TGGGAAAACATAAGTTAACTCAAGAATATATTCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98	C T C C T A A A G C	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAATTTTAAATGGAAGGACCACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCTCTAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118	A C	CTCAGTAACTCCGGTGTTAATCTGCCATTTATTGATTTTATGATAAAACACCTCTCATTTGTGA AAACAGCTAAGGGTGACATCTCCAGACCCAAACCCTGTCCTGTAATG[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A G A G G A A C A G	GTAGAGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAACAAACATCTCCCCAGGCCTCGCAGT AGAGCGGAAGGGAACAG[A/G]GCTGCCATGTGCTGTCTCTAAAGACGCCACCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C G	ATCTTTATAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24	A C	GCCACTGAAAAAGGTGCTCTCC[A/C]GTTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACITTAATCA
EST35164 8a	57	A G O O C C	CACAGCCCTGC O O C C	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCOCTAACAGATGACTCAGCAGGGCCTTCAAGCACAGCCCTGCCCCQ[A/G]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGTGCTCTGTGACATTTCTCTTG
WI-18052b	67	A G	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATC[T/C]GGTTACACATCTT[A/G] A/GACAGCAGAGCTGCCTGAGGGAGGGTGTGTTAATGTGTATGCTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATC[T/C]GGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTGTGTTAATGTGTATGCTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G A G A T A A A A	GGGAGTGGG G A G A T A A A A	CGTCACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[A/G]TGAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAG/GA/GAATGTCA AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGTATTATAGGTGCCAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	COCTCGGCACC TGCT	TTTAGCACCATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/C/JAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/C/JATATTACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTATTAGTTTGATATTTTCTGTACTCAGAACATTTTAGGTTGCAAGGATATAA
WI-18080c	80 C T	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTATC/TJTC/TATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCC/G/ AJTGTGGACTTTTATCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTC/T/CJTGTAAATTAATCTACTATGC CGTGTGGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63 G A	GTGGCATCCTATAAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATCTTCT/G/A/ TGGCTTTGTACACGGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGA
WI-18115b	71 C T	AACTACATAGTAGTGGCTGGCTTAGAATCAATGGGTAAGCCCTTTAGTGACCTTTTGGTATTCCT TTC/C/TJTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T	TTAGTGACCT TTGGTATTCCT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTAGTGGCTGGCTTAGAATCAATGGGTAAGCCCTTTAGTGACCTTTTGGTATTCCT TTC/C/TJCTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGGTGAG TCAGT
WI-18136	78 A G	TTTTGAGAAGCACTCTGTAAAGGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAATTTGC/A/GTAAAGACAATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAACT
WI-18169	115 A G	CCATCTTCCG GAAGCTC	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAGGTGTATCCAAAGCAGCCATCTTTCCGGAAGCTC/A/GTGGAGCACAAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A	TGAAAGAAGTCGACACAGCGGACACT/G/JTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62 G A	TGAAAGAAGTCGACACAGCGGACACTGTCTATAAGTGGAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAACATTGAAACACAAATACAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGTGAAATATATACAACACTCCCTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTTGTTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT CCCC	ATTGATACAAGCATTTCTGAGTACAAACTAGGGACAGGTATTTTACAAAAACAATAGAGCAGA GTTCTGCCCCTC[A/G]GTGCGGGGGGAGAGAGGGGATTTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60 T A A A	TGGTGTTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGTT[A/GAA CCCCTGAAACCTTTATTTTGAATTTGAAGTTTTGCTCAGAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTCTCTCAGTATTTTATCAATAGTGTAAAGCTGGAACCTTGAGTTTGAG ATCATAAT/CCTGTCTCACTAGTCTATTCACTTCTGTGGCATTTTCGGCAGAAAGTGGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCTTTCAAGCAAGTGAGGTCAGAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTT/CJTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A A	GCTGTCAGCTA TTGTTATTTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTTGGATATGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTTTC AAAT[A/G]TATCTCTGCTCCCTTTTCTCCCTTTTCTGGGATTCTCATTTCTGCATGTGTTATA
WI-18330b	68 A G	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGGI A/GJTAGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAAATAAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAAATTTTTTTGTTGAT TCACA
EST37564 5	85	T	CIAGA	AAATTC AAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTGAGGCCTCCATAGGCTGCAAAACACATCAAAAGGCATTAC TGTA CTGGAGAGGACTGAG
WI-18327	104	GA	TT	AAACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCACTTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	CT	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGGTTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	CG	GCATCAA	CCCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGCTGAGGTGGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCA TAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCTCAAGCTT GTGGACCAAGAGACAAGCC
WI-18012g	117	AG	---	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTGATCTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA	---	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTGATCTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTGATCTCTCTTCAACTTTCCAGACTTGGAAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTC[G/T]GTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTGATCTCTCTTCAACTTTCCAGACTTGGAAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	AG	CTCTGCATTG	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTGT[G/A]ATTAAAGTTTATTAAATCAGCTGACTTAGCATTTAGCATTTGGAGATTATCTGGAT

EST38512 7...	91 T G	TGACGATGCC AATACTTCG	CACTGCACCTCT GGGAAGC	TAATAAAACTGACCCAAATTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGT/G/GCTTCCAGAGTGCAGTGATAACTGTTATAGCC CCTGCACCTCCTAAAAGATCTTTTTC/TTCCTCCCAAGTCCTAACAGAAATGGTATATCTCTCTGAAAA AGATGAACGTCATCAATGGATTGTGTCTCTGCTCTGCTTTGAGTTTGTCTTTGTCCTTGAGAACCTTG TCTCCCTGCTGATTT
EST38519 0	24 C T T	GAACATCCCA TGTTCTGTTT TAAAGATCT	TCTGTTAGGAC TTGGGGA	AGTGGTCAAAATGTAAAACTAATGGGGACACCAAGCCCTCAGGAAGAACATCCCATGTTTCTGTTAA[T/C]TCTCTTATGTGTATACCTACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA OCATCTAGGACGGTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCACGCCCGGGGGCCCGGTGG AGTCTCGCGGGCCCGCCCTGCTCCGCCCTTC/G/GGCCACCATCCATTCCTCCAGGGG
EST38575 1	66 T C A A	GAACATCCCA TGTTCTGTTT TAAAGATCT	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAAATGTAAAACTAATGGGGACACCAAGCCCTCAGGAAGAACATCCCATGTTTCTGTTAA[T/C]TCTCTTATGTGTATACCTACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA OCATCTAGGACGGTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCACGCCCGGGGGCCCGGTGG AGTCTCGCGGGCCCGCCCTGCTCCGCCCTTC/G/GGCCACCATCCATTCCTCCAGGGG
EST38616 9	101 C G C T T C	GAACATCCCA TGTTCTGTTT TAAAGATCT	GAGGAATGGAT GGTGGC	AGTGGTCAAAATGTAAAACTAATGGGGACACCAAGCCCTCAGGAAGAACATCCCATGTTTCTGTTAA[T/C]TCTCTTATGTGTATACCTACCTTCCCTTCTCTTCTTATACACATAGATTTTCTTAATTGCAGC CCA OCATCTAGGACGGTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCACGCCCGGGGGCCCGGTGG AGTCTCGCGGGCCCGCCCTGCTCCGCCCTTC/G/GGCCACCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG CATTTC A A	TTGCAAAAATG AAGGAAAAA	TATAGTAGTACTTCTCTGCTGACGAGGAATATTACAGTCTGAACTGGGCATTTCAA[T/C]GCGTG GTATTTTCTCTTTCATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGGTCATTT TAATATATCA GTTTTTACA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTACATA[T/C]AGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTACCTGGACAGCCTGAGAGGGACATCCACCAGACCTACTGATCTGGAGTCCCA CGTCCCCA/G/AGGCCAGCGGGATGTGTGCCCTCTCTCTCCCAACTCATCTTTCAGGAACACGAGG ATCTTGTCTTCTGGAAA
EST38707 9	75 A G	ATCTTGTCTTCTGGAAA
EST38759 2	86 A G G T G A T A T G G	TGTTCTCCCTGA GGTGATATGG	TCACCATGCTG GACTTAAGG	TGACCTTGTATCTTCTACTAGAGGGGAGAAGAAATCACCTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG[A/G]CCTTAAGTCCACGATGGTGACCTAACTCAGTTTAAAAATCTTGCC TAGCAGCAC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT[A/J]TTTGAATTTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAATGCCCTTTCATGAGTAGGATCTCCTAAGTGGTAC AAACAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCCTAGCCATGCTCTTCACTTATGTGTGTTCAATCAACAAG TGTTATGAGAACCATTACACA[C/A]AAGCATGTGCCAGTCAGCAGATTCTGTAAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	TCTTACTGTGCTTACAACCTTCTCTCAAGTTTGGCGTGGTTTCCATATTTGTTATTTGTTATTA TTCAACACGAGTAAAAAGAAACTCATGAC[C/T]TCTCCTTGGACTCGCTCCTCTCCCAATCTCGAT ACCGACTGCACGTGG
EST38865 2	72 T C T G T G C A T G C	GCTGTAGAATT TGTGTCGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGAGTCTGTGTGTTCTGTGAGGAGCTGTAGAATTTGTGTGG ATGCT[C/G]CTGTGTCTCGTCTTCCCAATGAGCACATATGAGGGGAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA

EST38878 9	47 T	AAACATCATT ACTAGCCTAG C ATCCTAA	CCTTCAATAAA TCTCATGTCTT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTTCCC TTATCAATGTCTATCTCACACATTTTATTTTATTTTATTTTACCTTTTCAAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCA/GCJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	TTATCAATGTCTATCTCACACATTTCTTTATTTTATTTTAT/CJTGTTTTCACCTTTCTCAAAATATCGGATTT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TTTT	CA	
EST38899 5	47 A G	GCTAAACG	T	GCACTAACTAACTTTTCAATTTGTGGATTGCACAGCATGGCTAAACG/A/GJTAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACCTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	CAC	CA	AACTGAATGGCAGTGAACACTACACATCAAAACTTGGGAAATGTGGTTAGTGTGGTACGTTGAG GGAAACTTATAACCTCAC/A/GJGCTTTGTTTCAAAACACAGCAGACACAGAGATTTCCAACCTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	GGTGGG	CA	TAAACATTTCCCATTAATTTCCCTTGGTGGG/GCJGGGGGGGGTGGAGATTGCAGTGTCAAGATAAA TATCACAAATATATCAAACTTCAAAATTTGCTATGCTATTCACACACTGACATGAGCCACAAACATT CCTTTCACAGGGAAGTAC
EST39002 0	42 G A	TGACC	CTG	CCTGCTATGATGCTTGGCAGATCCCGAGCCCTTCGGTGACQ/G/AJAGGCTCCCTGCCAGGCTTGG CCCTGACCGGGCTCCACGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	CCTAAGGAAT	CGC	CACGTGGCCCTAAGTTCCGGGCTTCTCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTT/GJAGGGGACAGGGGGCGATGCCGCCAGCGAGATGGTCCGTGTAAGCCTGTGGTC AAGACCTAACTTCTGGA
WI-16398	90 T C	TCA	TTGATAT	AAAGATAATGTCTATCACACGCAACATATAGAAACATAAAGAAAAATAAGTATCCACCCTAAAAAT CCCTATTATTCATGATATTTTCA/T/CJAGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	ACT	AAAG	GGTTGTCTTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCTTTTGTCTCAATTTTAAACACTT T/CJTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAATTTCTCCAGTT
WI-16406	24 C T	AGG	AA	GCTTTAATGGCTACAGAAAGG/CJTGTTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTC	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGTTTTCATCTGAGAATAAACCTCCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATAATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAATTGTGCTGAGCCAGCAACCCCTCGAGTTACCCGGCCCTTTACCCACGCC AGCTCTGCTTGCTGCAT
EST39366 2	72 T C	AGAAACATTCTGTCTGATCAGAGGAAGATGTATGAGAAAATCAGAAATCTGACTGAATTCCTAAA ATCTAT[C]ACACTGAGAGGAAAATGGAAAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G	CATTGGATTA GGGTGAGG	TGATTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAGTTTATTTATGTGTGTAATTCACAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAAATGCTTCTCTTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G	ACAAAGTGACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTTCCCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGGAAGGCCCTCCCCGTACTCTCCCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCTATT TTCTGGGTGGGCCCTAGGTAATCTGTTCCTTTGGTCCACAGAGACAAATTAAGAAGATCAGGTCT GGCTGTTGC
EST39430 2	45 A C	GGCAGAGGAA TAAGTATGTT	CAGGGGTGCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTAGCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCACCTTTTGGAAAGAAAATAACAGGAACCTATTTATAT ACGTAAATCACITTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACCTGAACAGAAA TGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTT GTAGACATCT AACATTAG	CACITGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAGTTCAAGTTCAAGTCAAAACCAATTC
WI- 18387b	84 A C	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC[A/G]TTTGTG
EST40601	78 A G	TAACCCCAT	TGACCACAA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG
9	78 A G	GCGTGAACCT	TTCTTGAAGA	GCTATGTAGACATAAGA
		GAAACAC	AAGCGTC	TCCAGGATGTTTATCCAAAGCTGTGACCGTGAACATTAGACGAAAGAGGTGACTCGCGTGA
		AGTGATCAC		ACCTGAAACAC[A/G]GACGCTTTCTTCCAAAGAGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	ATCTTCAGGAT	GCACACCTTC	TCCATTCACTGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
		AGGT	ACACTGTA	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
		CATTCTGGTCT	AAACTGATTT	
EST43091	28 C T	TTATTTTGGG	GTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTTAACAAATCAGTTTTTCATAGGCAA
		CA	CTAC	CCTTTGAACATCAAAAGAAATAGAAATATTTTTCACAAATTTCTCATCTGTAATTC
WI-18420c	108 T C	TTCCATTAAAC	AAATTCTCAGC	AGAGAGACAACAAGAAAGAAATAGGGAATGGGAAGAACAGAGTGAATTAAGCAATCTTGA
		AGGAAGTTTC	ATTGCTATAAG	TTCCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA
		C	C	TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGA	CCAAGATTGC	AGAGAGACAACAAGAAATAGGGAATGGGAAGAAC[C/T]AGAGTGAAATTAAGCAAAATCTT
		AAATGGGAAG	TTTAATTTAC	GGATTGAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		AA	TC	TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
		CACCCTGTCT		CTAGACAGATTCAATGCACACAACAACAGGAGG[T/C]GGGGGTACACGGGGGAGAGCCAAAGAC
WI-18425	81 A C	AGACAGATTG	CCTCCTGTTGT	TAGGGC
		A	TGTGTGA	AGCTGATCAGCTGCTGTTACTGTGTTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
				CTAGACAGATTCA[A/C]TGACACAACAACAGGAGGTGGGGTACACGGGGGAGAGCCAAAGAC
WI-18449	129 C T	AAGTGGGACT	GTATCCAGA	TAGGGC
				AAATTGAGTCCGGGTGGAACATAAAAAAGAAAGAAAGAGAAGTAATCAAGGGAGGGCCAAAGTG
WI-18457	120 T C	GGAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCCTTTTGGCTCTAAGTGGGACTA[C/T]TC
		CCACAATGGC	TTTAGGCTTG	TGGATACAGTCAGGGGAG
WI-18462	39 A G	AGAGGTGA	AGATGGTTCT	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGCCCCCAAGACATTATTTTATTCTT
				AAATGTCCAAATATCTGCCTGATGTCTGTGTTGTGCACATTGGGGCCACAGT[C]AAATAGGCTAAA
WI-18476	60 C T	GAGG	GTGAOC	AGGCAGTCCACCTGCT
				GGTGCTATAGTCTGTACACCACAATGGCAGAGGTGA[A/G]TAGAAACCATCTCAAAGCCTAAAA
				TATTACCATACATCCCTCACAGCAAAAGTTTCTAATCTCGGTTTAGGGACTCCATTGAG
				TGAGACGTGTGACAAGTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG[C/T]GGT
				CACCTCCATCGTGGCCCTGGCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

WI-18491	109	G A	A A C A A T G G T A G G T G G T A T T	C G T G T G C A T T T T C T T G T A T C C	C T A A T G A G A T A C A T G G A G G G T T A G C A C A G T G C C T A A A C A C A G A T A A G T A A C C A C A A A T G G T A G G T G G T A T T A A T A C T A T T A T T A A T C C C A G A A T G A C [G/A] G G A T T A C A A G A A A A T G C A C A
EST50757 b	79	C T	G A G C T G G A G G C T G C T T C T	A C C C T T C A C C C G C C C	A G C C C C C T C C A C T C C A C T T G C T T C C A A A A G T C G G C T C C C G A G A G C T C G A G G C T G C T T C T T T T A T A T G T G C A G G G C C [C/T] G G C G G G T G A A G G T C A G A G A
WI-17675	103	T C	G G A C A T T T G G A T G G T G A C T T	G G G G A A C C A C C C A G G	G A T C T T G G A A G C A C T A G A A A C T A A A C A T C T T C A C C A G G T G C T G A A G A A A A G T G C T T C G T T T A A T T G C C A A G C A G G A T G G G A C A T T T G G A T G G T G A C T T [C] C C T G G T G G T T C C C C A T A G A T T C A C C A T T G C C T C T A A T G G T G T C T A
WI-16543	67	G T	A G A T A A A C T A C A T T T G G G T T	G A T T C A T C A T T A C A G G G A C T T	G A T C C A T T A C C T A G G T A A A T T C T C T G A A T G T C A A C A A A G A G A T A A A C T A C A T T T G G G T T T G G [G] G [T] A A G T C C C C T G T A A T G A T G A A T C A A G A A T C C T C A A G T C T G T C T T G C C A C C C A T T T A A T A C G T A T T T T T G T A A G G C T G A A G T T
WI-17687	107	C G	G C C A A A A A G G T T G G G G A A	T T A C T T T T G T A C C G A C C A G C A	A T C T G A G A T G G A A G A G T T T C A T C C C A A A C C A T C T C C C C T G A C C C C A G T C C A G T C C A T G G A A A A T T G T C T T C C A C A A A C C G G T C C C T G G T G C C A A A A A G G T T G G G A A [C/G] T G C T G G T C G G T A C A A A A G T A A T T G
WI-17690b	79	A G	A C A A C A T G T G A A A G A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T T C T A G C T G T G T T G A T T G G C T T C C C T A T A [G] A T T C A G G A C C C A T A A C T C T T G T T C A C T A C A T C T G A T G C T G C T G
WI-17690a	63	G A	A G G C A T T T T T C T A G C T G T G T T	C A A G A G T T A T G G G T C T G A A T C	A C A A C A T G T G A A A G A G A T A T G T T G T C T T A C T C A C A G T G G A G G C A T T T T T C T A G C T G T G T T [G/A] T T T G G C T C C C T A T A G A T T C A G G A C C C A T A A C T C T T G T T C A C T A C A T C T G A T G C T A T G C T G C T G
EST51717 b	128	C T	G C G G A A G A C A G T G A G C T G T T	T T G A G G C A A T A A T C C A G C T C	G A T C C A A T C T C A G T G T C T A A C T A C A T C A T C C C A G A T T A T T [C/T] T G A A G T G G A A C C A C C C T C C G A C C C C A A T G G C A A C A T C A C C C A C T A C C T G G T T T T C T G G A G A G G C A G G C G G A A G A C A G A C A G T G A G C T G T T C G A G C T G G A T T A T T G C C T C A A A
EST51717 a	39	C T	G A T C C A A T C T C A G T G T C T A A C T A C A T C A T C C C A G A T T A T T [C/T] T G A A G T G G A A C C A C C C T C C G A C C C T T T C C A G G T T G A C A G G T T T A T T C C A C C C C C T T C C A T C C C C A T G C C C A C C C C A G G C A G G A G A C A G G T G T G C T G G A G T C T G G T C A C T T T G G G G C C [C/T] G G C G T G G C A G A G C C C A C T G G G T T T A C A T T C T C T G T G G G C A G G T G T G A C A C
EST53012	97	C T	T G G T C A C T T T G G G G C	G G C T C T G C C C A C G C C	T T T C C A G G T T G A C A G G T T T A T T C C A C C C C C T T C C A T C C C C A T G C C C A C C C C A G G C A G G A G A C A G G T G T G C T G G A G T C T G G T C A C T T T G G G G C C [C/T] G G C G T G G C A G A G C C C A C T G G G T T T A C A T T C T C T G T G G G C A G G T G T G A C A C
EST53349	96	A G	T G T G A A A G C A G T C A C A A T G T A C	C A T C T G G A T A T C T T G T C A C A T T T T	A A A C T G C A A A T A C A A A A C A A A C A G A A G T C C A A G A G G C T A A A G T C T A A G C T A T A A T T A C A C A T G A A G T A T A T G T T G A A A G C A G T C A C A A T G T A C [A/G] A A A A T G T G A C A A G A T A T C C A G A T G T T T A A
EST53389	74	A G C A	G G A G A C C T G C A G A A C T T A A A	G C C C T T T C T A A C A A T A A A T G C T C	T T T C G A A A T G T C C C A T G A C T T G A C A G A C T G A G A G C C A G C C A G C C A G C C A G G A G A C C T G C A G A A C T T A A C A C [A/G] A G A C A T T T A T T G T T A G A A A G G C A A G T C T T A C A C T C A A A T A G G T T T T A A C A T G A A C A C A T T A A G G G A G A T G G C C

EST53477	61	T C	CGAGATTTCT TC TTTATTTA TATTTTCA	CCAAAGAAA TGGCTTCAGTA A	TTTGAGAGGTTGTGCAAAACTACTGTATTACAAAAATGGCACAAAAGTGAATTCACAGTT/CJAA TGCACATGCATACCTCATTCACATCTTCAACAACAAAAGGTATTCTAACTCTACAGAACTGAATATT AGCTTCAACGGCAGCTGT
EST64622	91	T C TATTTTCA			A	TGTGTATAGCA CATACTTCAGG	ATGGGGTGGTG CCGC	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTTTAAACTCCCGAGATTTTCTCTTTATTT TATATTTTCATTTTCATCCTAA/CJTACTGAAGCCATTTCTTTGGTTAACTTTAGA
EST67268 a	77	C T C			GCAC	ACGACGCCGG CGAGT	GCATTCOCGG GCAC	CTCATCTTTATTAATGCATGTATAGCACATA CTTCAGGC/CJTGGGCACCACCCCATAGAGATGGTGAGGAAGTAACCTTCTGCTTCTCATTTGAAACT GTAGATCCATCGGGGA
EST78503 a	26	C T CGAGT			...			GAATGCAGAACGACGCCGGCGGAGT/CJTGTGGACCTGTACGTGCCGCGGAATGCTCCGTTAGCA ATCGCATCATCGGTGCCAAGGACACGCATCCATCCAGATGAA
EST80253	92	G C	ATGCACTTTATTGGTCCAGGGAGTGGGATGCAGGATCAGAGTGACACGCGCAGGGGGCTGGTGTG GGGAGCAAGCGCGCGCTGCC/CJGGACCCTGGTTCCCTGAGGAACCAACGTGAATGGGGGCC CACTGGAAGATGCTTG
EST91254	73	T G	TATCTGTAGGGAGAATAACCATGCTTGCTTATGGACTATCCATGGATAACTGGTTTTTGTGTGTG TTGTTT/GJTAAATTATAAGAATAATATGTGCTCATCATATCAATGOCCTTCTCAGTAGAGCCCCAG ACCTGG
EST91332	100	T A	TCCAACTGAAAGGAGGGTGGGAAACAAACGCATCATATGTAAAGCACTGAGTCCAGCCTGGCTC TTAGTAAGCATTTTAAATCACCTTCAAAAATTAA/CJTGTGACTACGGAACAGGTCACTGAATAT TATT
EST91495 b	58	T C	CTGACTCAAAGACACCTCTGAAAGCAGGTCCATCCTGAGCAGCAGCTTGATTAATCTT/CJACAAG TCAGACCTGTTATTAAGACGCAGACTGGCATTTAAATCAGGCTGTGTACACCCATCCTGGGCTCTT GTTCTGGCTCCTATGGTG
EST91921	114	A G	CTGGCTGAGGATCTCAAAGACATTCACCACATTTGAATCTTAGGCTGGAGGACATTTTCGTAATCT CAGTCAGGAATAGCACACTTCCCTTCATGAATAGCAGCTTTTAGGG/AVJTTATATCATGAGGTACA AATAAGAGGCCCTCACC
EST92026 a	56	T C	ATAGCCAAGATTTGGAAGCAACCCGTGACCATCAACAGATGACTGGATAAATAAA/CJGTGGTA CATGTACACTATGGAGTACTATTACGCCATGAAAAGTCTAAGATCTTGTCAATTAGCAACAACATGG ATGGAACCTGGGAACACTGT
EST92040 b	38	C T	TTTCCATGAGGAATAAATTTGTGTTTATATAAAACCTG/CJAGATGAATAATTTTTTAAACAGCATG ATTCACAAATGCCAAAACAATGCAAAATGCCCTTCAACACATGAATGGATTAACAGACCGTGATAC ATGA
EST98276 c	69	T C	GAGTCTTGCTATGTTCCAGGATGGCTTGAGCTCCTGGTTTCAACAATCCTCCTCTCTAAGCCTC TT/CJAAAGTGCCAGGATTATAGGTGTGAGTCACA

[illegible]

TGR- A003P30	117	C G	---	---	ACAAGTCAAAGGAGAACCTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCTGTGATTTCCCTAGGA AACCATCTGGGTTTAGCCCATTAAGAAAATGCAGTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TGR- A004S34	158	C T A	---	---	GCTGTCTTTTATGTTTAGTTGCGGGGAAAGGAGGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCAGGGGAGTTGACAACTTCTTTGCTCTGGCTAACAGTCTGTGATGTGACAATAGCCA AACCTCCTCATCTCTATAAA[C/T]CTTTAAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C	---	---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAAGATCAGGAAGATAAACCCAAAATGAT TGAGTATGATAAGAAATTTGCATGGCGATT[C/A]AAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004T44a	69	G A TGA	---	---	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAAGATCAGGAAGATAAACCCAAAATGAT TGA[G/A]TATGATAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TGR- A004V08	60	T C	GGCATTCTCT	AAAGGC	CCTACAATCCTATAATATTGCAAGGGTGGGAAGGATGCAGGAAACAGGCATTCTCTTA[C/G]GCC TTTTGTGGGAAGGATCAATGGGTGCATGCACITTAGGGGACAAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TGR- A004V26	125	A G	---	---	TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAATTATCCAGAATAATCTCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTACATGA[A/G]AAGGT TTCAGTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TGR- A004V28 a	29	A G	CGATCTC	CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGGGTGCGATCT[C/A]GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAAATTTTG TATTTTATAGTAGAGACATTGTATTTTATAGTAGAGACAGG
TGR- A004X20	25	T C GA	---	---	TAAGTTTCTCTCTCTCTGTAGGAT[C/G]CTCCTCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACTCTGGGCTCGCTTCAGAGGAGTTTGATATTTGGAGTGGTACCTTTGTTCTGTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCCAATC ATCATCATGTCTCT
TGR- A004X30	26	T C	CCAC	CTATTTT	TTTTGAAATCTTAGAGTAGAACCCAC[C/T]CJACTCTAGTAATACCTTGTAAATAAAATTAATAATAGTTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G	ATGCAAAACT	AAGCAA	CACGGTATATGCTTATATATAGGTATATATACAGATCGTACACAATATATTTACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[C/G]TTGCTTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTTCTTCATATTCATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTCTCCCGATGACCAATCTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGTCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT T AGGAGACT	CAGGGCTGCCG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCAAGGCCAGGTAGCCTTCAGGGGGGGGCA GGGTTGGGGGAGGTAGGAGACTCTTGACCCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTAAAA CTGTACAC	TTGCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAATTTGGTCACTCAACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACCTGTTACACTGTGTTTGGCTTTAAATAATAGACAATGATTTTGG TCTATTACTTAGTGATAGACAAAGTATTACTTTGTAGACAAAGTATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAAATTTATAACCGCCCTCTG/AJCTCACAGCTGACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTGGCTGTGGCCCTACAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTTGGCTCTTATTTGTCTTTTCAACAGGACC CCACAGATATTTGGGGTATGTCTATGAGGACTGGGGATGTCTTCTATTG/CIGGATGTCTTCTATTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGTTACTGCACCTTACAGAG/AJCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATTCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAATAAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/AJGTACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCAACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACCTTTGTCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCTTTGATATTTGTAAAAATCCCCCAAGAGCCGCATATGAATCTGCCCG

X57830	106	G C	CT	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	A	GTGGCAACTGTGGAAAGGCACACTGAGCAAGTTTTTACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATCTG/CJTATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G	TGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC	TAGATT	AACCTGAAGAAGTTACTGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TGJGATAAAAATCTAGATCTCTAATAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTT CAGTTTTTGTCTTATACACAATTCATTCTTTGCAGCTAATTAAGCCGAAGAGCCTGGGAATCAAGATT GAA
Z48804	44	C T	---	---	---	---	ACTGCCAAGTGTAGCGGCCCCCAACCTTGTCTCTCATCCAG/CJTJAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGTTTCATGCACACACGCTGAGAAATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	---	---	ATGACCAAGCCACCACATTTAGAACITTTGGCTGCCCTTTGGAAGTCCAAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTTGATTGACTGCATGAATGCJA/ GJTGCGTGAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	---	---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTTCCGACCAAGACCCTATCCACCTGGACC TCCATTTTTCCCTGTAJA/GJTTCTCCAAGTATCCTACCCCTCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAAAGACACCACTACCCCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	---	---	CCACTCCATCCTGATGCCCAJA/GJTTATCCACAGCCTCCTCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTTCTCCAAGTATCCTACCTCCTCCTCCTCCTGCAACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAAAAGACACCACTACCCCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	---	---	CTCCCTGCCCTCCTCCTCCTGCTGATGCTCCGCTCTCAACAGCCGAACCTGCTTGCATGGGGG GAGGGGGGTTTG/AJCTTTCTCTCTCTTGGCTTCTCTTATTTCCACAAACCACTTCTCAATAAA GCCAAAAATCTTTCTCTCTCTCTCCCTCAGGCCACCTCCTGCTCCTCACTCCTGCTGCTGGCTTTT CTGGA
D327031	64	T C	---	---	---	---	ATTATCGGAGTGTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTTGAGCTG/T/CJ/ CCCAGGCTCTGTCTCCTCAGCTCAATTTCTACTCTTTTCTCTATATAACTCATTTCTATAAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTATAAAGCTTCC TTT

D63807	101 C T	CAGCAGGACTTCAGTGCAGTATCCCTGCCCTCAGTCTCTTTAGAAATCAGATCTGTGTTCAATCC ATTGTTAGAGGGAGTGATTTTCTCTGTTCCA/C/TAAGAGGAGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTTCTCCCGCTGGCTCTCGGTGCTGGGAGGGTGACCTGTCCAGATGAC. TGGGAACATGCGTGTGACCTC/CJACAGCTACCTCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTTAAATTTTAAATTTATTTATCTATTTAGTTTATTAATTTATTTTGTAT TTCACAGTGTGTTTGTGATTGTTGCTCTGAGAGTCCCGCTGTCCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21 T C	ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAAGTACTTTCTTATTTATGAGCCCCCT/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTTATACCATCTAAT
EST14035 1a	59 T C	GCATTTTAAATTCACATTGAATCATTATTACTATTTATGATGTTTACATAACAAATTCAGTATCATT ATG/C/TJTGATGTTTCAGATGTAGGTGCTCAATACTGAGCACTTATCT
EST16668 5	71 C T	ACAGACTATCGCCAACTTATAATGCTTAACTTTATGATCAATAGTAATAAATTAACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTGTGTAAGATGATTTTCCCACTGTAGGTTAACAT
EST16904 7	57 C T	TTTTAAGTACCAGAGGCACGTCTGGAACAGGATGAAAACGTATACACC/CJGTTACTACTTACTC TTCACCTTTCAAACTGATTCCTTAAGACTTCTACTAGCAAA
EST21863 9	49 A G	GGCTGTAAGTAGAATCAAAAGTTAAGAACATTTTATGCACTTATCCACAAACATTTACTGAGCATA CTAGGTGCTGGGA/C/JTGTGACAGTGAGCAAAAACACAA
EST21885 6	80 G A	ATTTTAGTGCAATGACAAAGCCCAA/CJGAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22623 8a	26 A G	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/CJGAAATGTGAAAGATGGCTTTTAAACCC
EST22644 2	98 A G	CCTCATTATTTAAAGACGGACATAAAAAT/CJATATACAAACAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31 T A	AAAGATCTGGCATTATTCACATCATCTCTAAATATTTTGTAAATTTTCTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/CJGAAATACCCATAGTTACAGAATTGG GTCGTGTAACTCAAT
EST24246 7	106 T C	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/CJGATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24308 3	45 A G	CTTGAACCTCTGGTCTCAAGTGGTAGCTCCGTCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/CJG/JTGCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73 G A	TATTGTTGCATTATCAAAATGGTTA/CJAGTTTTCAAATTAACCTGTAATTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT
EST25089 6	25 T C	

EST25476 9		33 GA ...	AATGATCTTTATTTTTAGACCTGCTCCTAAAG[GA]CTTTCCTCCTCTAAAAAACCAACAACA AGAGGTCTCTTGCTGCCCTTCCATGGACTGTGGCGCTGGAGCTTGGACCGTCTGCTGA
EST26183 2		70 T A ...	AGATAATGCATTAGAGCCTGCCCTCATTTGTATCTTGATTAACTTTGTAAGAATTGATCTCTAAATAA ATT[A]ACATTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a		28 TC ...	AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTCTTTTAGGCACATATTATAGCAATT CAGATGAAGTCTGTAAATCACACACACACTGTGCCCTAACACAACAACACGGTGACTCTGA
EST27816 5a		26 TC ...	CAACTCAAGGTACAAGACAATTGCATT[C/T]AACATTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCATGTT
EST28588 0		78 AT ...	GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTCTGGGGAGGTCTCAGGAA ACTTACAATCAJATJGGTAGAAGGCCAAAAGAGAAAGCAGGCATCTCTCCATGACCCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5		25 AC ...	TACTCACACCGACATACATATCTCA[J/C]GTAGAATTAGCTATACTGCATATAOCTTCACTTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a		59 CG ...	AGCTATGGTAGAGCAAATTCAGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/GIAGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7		25 GA ...	CCGAATATAAGGAAAAAATGGTGGC[G/A/JTGCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCAGTTCCTATGAATACTGGCACTGTTTATTCATGTTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4		27 TC ...	TGCTTTGTTCCCTCCAAATCTAAAA[T/CJGTGTCTTCAAAAGAAATTCGTGGAAAGGACTTTTGAA TACGAGTTGTACCATATTCAGATTCTTGAAATACAGGTTTCAGATACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b		75 CG ...	TACACATTATTCAAGAGACCACTGACATGCATCTCTCCGCAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTTTTACTAAGAGAAATATCTTTGGTGCTATATCTAGGGG
EST33424 1		126 AC ...	ATTTTCCCACAGCAGAGATATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAACAAGATTACAAAATCTCAGTCAATTACACACTGAGCAAC[N/CJAAA CAAAGGTGTTGAATCCTCTT
EST33488 7		90 AG ...	CCTTTGGGGGAGTTTTAAGCCAGAATGTGACAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACCTAACATCGTCTATAGJA/GJACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b		45 CT ...	AAAAACATGCTATTTGAACAAACTTTTTTATAAGAAATAAGTTGA[C/T]TGAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508	36 A G ...			AAAACATGCTATTTGAACAAACCTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT
1a			...	AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863	77 C T ...			ACAACATAGGACTGGTTATCTTGGTTTGAATAATATGTTGCCACTTCCTATTGTTTTAAAAATGA
4			...	TCATTTAA[C/T]TCTTTGAACACAGCCTGAATCCCC
EST34739	97 T A ...			GAAGTATCCTTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCCAGGTTGGACCTTTTCGTTGATGA
3			...	GCTGATAGCTTCTAGGCTGGGGAACTCT[A/G]GTGCTTACAACCTCAACTACTGCAGAATTTCT
				TGTTGGCCCTCATAAACA
EST34792				ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCAGTGGCATCCACTATCAATA
6b	104 A G ...			CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTGAGGAATCTTAGTCCTATTACA
EST34835	93 T G ...			AAGATTTTGTGCTGTG
9b			...	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST34835	82 G A ...			TGGGAGTCTATGTTGCTTTCTGGT/GGGCTTAAAGAAACAGACAAATTTGTCTAAAGAT
9a			...	GGAAATGTTCCCTTGCACAAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG
EST35230	93 G T ...			TGGGAGTCTATGTT[G/A]TCTTTCTGGTGGCTTAAAGAAACAGACAAATTTGTCTAAAGAT
0			...	CACAAAGGTCACCTTACTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG
			...	CAAGACATGAGCATAAAAGAGGTTCTC[G/T]GGCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337	33 C T ...			TCTTTCAAATTTTGTATGAGGCATTTAATG[C/T]ATAAATTTCTGCTTAGGAATGTATCTGCT
9			...	ATATCTCAGAAGTTGGGCATGTTGTTTCCATTTTACTTAGTTCAGAACCTTTTCAATTTTCATCT
EST35708	32 C T ...			CTGCCCCAAATTAACCTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG
9			...	ACAGCTTAGTAATATGTCATATGCAGCGTTGCTTCCCTCTCTGAGGTTGGCACCTTTCCCTGTTGTG
				ATGTGCAAGTGTGGCT
EST35747	51 C G ...			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAGGCTCCA[C/G]ATGTTAAACGT
9			...	TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCTCCAGTAGGGTTGAGATT
				G
EST35751	89 C A ...			TGGTCCATTATATAAACTGAGGGAACAAACGGTGTGACATGGCAGACATTTATTTCAATGGAGA
9			...	AGTTCTCCCATGAAACCAAGAC[C/A]CTTGTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT
				ATATAATTAAAGCCTGTGA
EST36301	93 C T ...			CACCTGTTCAATGGTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTAGCCTACAGC
4			...	AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA
				GAAAGAGGTACAACAAA
EST36519	33 G T ...			GCCATCAGCCCCACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC
0a			...	CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT
				CACAGGGGCTTAGTGTG

EST36620 6	50 G A	GAC TT TATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G	CCTGTGATGTGCATGGTGCTCCTGAGCAGTCTACTTACTATGCGTCAGACAGCTCACGTATGTCTAGGA AAGGAAGTCTGGGATTCTTA[C/G]AGGGGACATATACACATATTTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCTTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACITTAGCTACCTGGACAATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103 A T	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATTTATTTCTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G	ATGATCGCTTATGTAAATTTGAGGGCGACATGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAAGTACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAAATGCAG
EST37054 3	88 T C	GGTCTCACTCTCTTGCCAGGACGGTTTGAAGTCTCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGGTT[C/G]TGAGCCACCACACCTGGTCTTGTTTAAAGTAAACCACCTGAA C
EST37269 3b	105 T G	AATAGTCTATGGCTACGGGCCGTTGGAATTTAAAAATTTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[G/C]AGGAGAAAAAATGGGGTCC
EST37284 2	93 G T	AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAAAACCTTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G	AGATGGGGTCTTGCTAGCTTGCTGGGCTGAACATAAGATATCTCTGCTCAGCTCCAGGTAGT TGAACTATAGTAGGAGTATCTA/GTCCCTGCCCTGCTAGAACTTCAAGTTTGATGGGCAAAATCCA CCCCAGAGCAGGACAA
EST37374 1	45 C T	CCTGCCATGATAATGTTAAAAATATCAAGATCCTCCTCAAACTT[C/T]AAGGGTGAAAGCATACC ATTCCATTTTAGTTGAAATATTCTTACATAGCCCAACACATTTTTTCAAGGCACCTCTAGCTACTACA GGA
EST37376 8b	101 G C	GTGACATCATGCTCTTCAATGCCCTTTCAATTAATAGTAGTTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGCTGTGCTCTGCA[G/C]GCTGCTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41 T C	GTGACATCATGCTCTTCAATGCCCTTTCAATTAATAGTAGT[C/T]GAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGCTCTGCAAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCTGTGAAAAAC[T/G JAACATGCCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A	AAGACATAAATCTGCAATGAAATCAGTTATGAAATATTAACCTCTG[A/CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34 A G	CTAGGCATGGGCTTTACAGTCATTTATTTACC[A/GTGCATGAATTCATTAATAAACACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATCACCCGTGCTCATGGATCTTCCATTCTAA
EST38025 4	56 T G	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATACACTTA[T/G]TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTGAGAA
EST38068 6	57 C T	TCTACAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/TCGCATGG AAGAAGCTCTCCTTTAATCCCTAACTCTCTTCTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C	TAAATCAAGGCCTCTTTTCAATCCAAACAAACAAAAAAGGGAACAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTCTCATCTGACTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C	TTATTGCAAAAGTAAGCAGCCGG[T/C]GGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACCTGGGACTTACATTTGACACAGGCTAAAAGTATGGGATGAGAGAGGAACAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C	TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGTTTAAATATATCATTTTATGGGATGAGATCA TAGCTTTACACAATGCTATG[T/C]AAACAAGTTACTGAAATATTTTACCTCGTGGAGTTG
EST39331 1	70 G C	TCCTCTTGCTCTAGCACTCAGACCAACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TGC[G/C]GTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTCCCTCTGCCATTGACCAGATGGGT GCCCTTGGATACATCACT
EST40544 7	31 C A	GTCACCATTGACCTTACATAGTGCCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACCTCTATTGTACTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C	TTCTAATAGCATGCCCTGTGACAGGGGAAACTAAGCTC[T/C]TCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAAATTGAGAAGGCACATGCCCTTTGTAGTTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G	TGTTCTCTAGAGAACCCCTGTGTGATACACTACGCATGCACA[A/G]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTGTTTACCACCATTTCTCACTTTGAACCTAGTCCCTGCAAGACACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAITTTTCACTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTTCCAGGAAG
EST40584 3	68 A G	TTGTATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTTAAGCT

EST51340	51 G A		GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACTAAGAGCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04162	134 T C		CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCTCTCTACAAGCAGCAGGAAACATAGAAGCTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAAGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCAAGTGAAGT AGCTG
K01506	63 T C		CTGAACCTCAGCTGCCCTACAACTCCATCTCAGCTTTTCTCTCACITTCATGTGAAAACTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCTTCAAGCTCTGCTCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTATCCT
L18877	69 T C		TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGCCAGTGCACCTTCCAAAGGC C[T/C]ATCCATTAGTTCCACTGCCTCGTGACATGAGGCCCATCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTTCTTCTGTTGGA ATTGTTCAAAATGTT
L31848	36 T C		GCTATTTTACATATCCCAAGCCCTTAGGGCTACAG[T/C]CTCTTCTCCTGGACCCCTGTAGGGTGCCA TTTGGAGTTACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGTGCGATAGGCCTGTAATCGT AGCGCTTGAGAGGCTGAGGCCAGGAAGATAGCTTGAGCTCAGGAAGTTGAGACAAACCTGGGCAAT GT
L38517	137 G C		GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGCAACACAGCGTCCCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G		ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTTGTATAT[T/G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGTGGGCTGTGTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173 G A		CAAAGTTGTCCTGCCCATGAGCACACAGTCAGGCCTTAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACCACACAAATCTGAAC[G/A]TGCCTCTCCCTTGTCTTACAAATGTCT AAGGT

L48728b	111	T C	...			AAGTGAACAGAAAGCATGGATTGTTCTCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAATC/GAAGAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTTGGAGATCCA GTC
M18079	52	G A	...			GCGCACAGTCCAAAATACAAATTGGACAGAAGATCTATATTGTACCAGAACT[G/A]TTTATTTCAACC CCATCAAGTATAAGGTTACTGATTGGTCTCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAGTAAAGCTAA
M19169	113	T C	...			TAGGGATCTGTGCCAGGCCATTGGCACCCAGCCACCACCCCTCCACCCCTGTAGTGTCTCCACCC TGGACTGTGGCCCCACCCCTGGGGAGGCCCTCCCCATGTGCTGTC/GC/GCCAAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114	T G	...			TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAAAT/G/GTTCCTTTCTGAGGCTG CCATGTCGCACGTGCCAGGTGAGAGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G	...			CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTCTCTCAAGTGTACCTACTAAG[G/G]GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G	...			CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGACTTC CTGATTTTCTCTCTCA/G/GTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G	...			CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCTC/G/GCAAAATGTTTCTCTCTCAC TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTTATTTCCCTGAC TTCCTGATTTTCTCTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C	...			TAAGGCAGCTGTCAAGGAGGCCAGTCCAGTCCAGCAATTCACAAACCCTTGAC[G/C]AATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCCTTTCTTTGTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCAATC
M81695	34	G A	...			ACTTACTACCCCTCACCTGTCAAGGTGACGGGGA[G/A]GAACCACTGCACCCAGAGAGGCTGGG ATGGCCTGCTCTCTGCTTTGGGAGAAACGCTTGTCTGGGAAGGGCCCTTTGTCTGTCAAGGTT CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTCTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U08641d	166 C T	CTCCTCCTTTATTTACGATGGAGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTTAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAATTT TATTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATTAATCTATGTCATGATTTTAAAGCTA TGAAATACAATGGGGGA
U09607	39 T C	GAGGCCTATGAGGGTCTCTACTTCAGGAACACCCCA[C/T]GACATTGCAATTTGGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGTTCAAGACAGATGGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGCAAGCAAGCAACCAAAATTAAGACTCTCGCATCTTCCCAAG CCCTTA
U09608	82 T C	GAGCAGAGGCAAGAGCGGCAAGATGAGTTTGGCGTTGTATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[T/C]ACATCTGCCCGCCCTCCAGCCCTTCCCAAGCCCTCCTCTTGTCTTCTC ATTCAATCAACAAATTTGGC
U10694	20 C G	GTGACATGAGGCCCATTT[C/G]GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTGACCTTGACAAAGTTGTTTAAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCCAAGAGAT[T/C]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C	TTTCTGCCACTTTTCACTGGTTTAAATAGCCAGCCAGTCATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[T/C]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122 T C	TCCAATTATTGGTCCCAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAAAGTCCACGGGATTACAGAACGTCCTTGACAGCTGAGCGATGACACCACAC[T/C]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACACTGTCTCTGG AATTA
U18543	58 T C	GCACATGCAGAAATAGACTCAGCCTATGTCCTGATCCAGCTGGGTAGTTCTAGAACTTT[C/J]AGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCCCCTCCCGGCTCCCACTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACAGATGGTGTAGCTGAAGTTTATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A	---	---	---	TCACTGCTGGCCCTACTACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G	---	---	---	TCACTGCTGTGGCCTCATCTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G	---	---	---	CAGGAGAGGTTATTCAACAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCCCCTTAAAGAAAAATT GCATGAAACTAGGCTTCTGTATCAATATCCCAACATCTTGCATGGCAGCATTCACCAACAAAAA TCC
U28413	29	C T	---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89	A G	---	---	---	TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGCAGTGATGTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAAACTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34	A G	---	---	---	TAGGGGTAGCATTAAAGATTACAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78	A G	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTCAATCA[A/G]CCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCCCAGCGGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A	---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCC[G/A]TCATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCCCAGCGGATTCGCTTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	78 GA	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAG[G]CCACAAATCTGGTGCCTCTCTTGCTTACAAATGTCTAGTCCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]/TTTCCTACGCCACAAATCTGGTGCCTCTCTTGCTTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT	ACGGGTACACAGAGAAACCTGAGCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTCTCTCC AGACCGCAGG[C]/TTCCCCAGCCTCAGGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTTGCTTCTATCTGGGGGACGCTGCTCGAGAGGCGGAGGCGCGAGAAC ATGCCAGGTGTCC
U37690	54 AG	GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G]/CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCCTT
V00540	39 TC	TGAAACCGTTTCAACATGGAATGATCTGATTGACTAA/TJACACCAAGTCCACACTTCTATGACT. TCTGCCATTTCAAGACTCATTTCTCCTATAACCACCGCATGATTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT	TCAAGAAGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGGTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAAAAA/TATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAAACCCTGAGATCATCAG
X52011b	148 CT	AGGAAGATCCCACCGACCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAGTTGCGAAAATTGCG AAATCTGTTGTGCA[C]/TJGCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A/C	AGGAAGATCCCACCGACCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGCAGCTCAAATGAAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTTCTCTCCACAG/GTGCACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAACCTCCAGGGCTCCAGGACTGGGCTTGCAGGCTGTCAATAGCAAGGCCAG GGCAGACTGGAGACGATCTTGTGGCAGGGCTGGGCTTGTCCAGCCCCACCTGGCCCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTCGGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAAAATGAATATGTTATTTGCTCTA/GJATACAAAAATCTAAATCAATATTGAAATAG GATGCACACAATTAATAAGTACAGACATCTAGCATTTGTGCGGGCTCATTTTGTCAACATGGTA
X68924	147 G A ---	---	GGCGTGTCTGACACCTCCAGAACGAGGTGCTGGGCGGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCCGGACGGCAGGATGGGCGCAACTTCCGCTTGGCCACTTGACTTCAACCAATCCCT TCCTGGAGACTG/AJACCTGGTGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAAATGTGACAAAGCCTTTAAGCGGTTGTACACACTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAAACTCCAGAAAGTGTGACAAATGTGACAAAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTATACTTTGAGAAAAATGTATAAAGAAATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTCAACCCATAACCTCAACACATCT/GJATCTCTCCACCCACATCCACCCACATCCACCTCCATCC CCAACCCATCCTCATCCCCAATACAGCCCCAAACCCAGCCCCAGACTAATCCAGAGCCATCCCCAA CTCATCTCATCCCCAATGCAGCCCCAAACCCACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99 G C ---	---	ACCCCACTCAAGTCCAGGCCAGGCATCTTCTGCGCTGCTTGGCCATCCAGTCCAGG CGCTGGAGCAAGTCTCAGCTACTTCTCTG/CJACTTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCCACTCAAGTCCAGGCCAGGC/GJCTTTCTCTGCCCTGCCCTTGTGGCCATCCAGTCC AGGCGCTGGAGCAAGTCTCAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCAAGTCCAGCAGGAGGGCGCGCTGCGCGTGTCCGTGTTTCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCCAGCCTCAGTCCGACGCTCCCGCGCTCT CTTTCTCCCAAGC/G/AJAAACCAATGCGCCCTTCACTGCGTGTCCCGTGCAGGCCGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGCCCGCAGCGTGTGCACAGGGGACCCCTGCCCC CACTCTGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GGGGC ATGCGCAGGAGGAGCCATCGGGTACTACGCGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA

[illegible]

1282	130 C T	GTGGATCACCACACTACAGTCTAATTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGTACCCATTAGAAATTATTCCTCATCTGCCCCTACCCCAGGCCCTACTCTTTATCGCTATAGATTTGCCCTGACTTGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTCTTTCACTGAGAATAATGTTTTCAAGGT
6810	68 C T	AGTATCACACATACITTAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTTA/C/TJAGAAGCATTTTAAATTTACAACACAAAGCTCAACGAACCTACAATAAGTCTAGTAGTCTGTGTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGCTATGAACAAGTAGCAATTTCTTTTGTGCTGTCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
6817	118 A C	CCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTATTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGAGGTAAC/A/CJGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTACGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTGCATATACAAAATTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACITTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T	CCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTG/CATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACITTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTAG/TTATACTATGGCACCATTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCTATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATTCG CACAATTCAGAG/C/TJCCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA/A/GJCTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208 A T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192 G T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCC[G/T]ATTTT CCTCAATGCAGA
7598h	144 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACAGATTTACCTTGGAGAAATGAAAATTATTTCTTG[A/G]GGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA/GJAGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTCCCTGATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G	AAAGGTAAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCAAGGAAC TCAATGAATAAGCCGCTAACCCAGATTTTACCTTGAGAAATGAAAATATTTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTCTCAAGGTCCCAATAA/ATCCTTGAGGTTCCCT
7998b	94 A C	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTA/CJTCTCAAGGTCCCAATAAACCTTGAGGTTCCCT
7998a	75 A T	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTATTACAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTCTCAAGGTCCCAATAAACCTTGAGGTTCCCT
8071	119 A G	AAATACAGAAATTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC/A/GJCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTTCATTTTGGCATTGTTAATCACTGAATC TGGGTTTCCCTCTGAATTCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAAACTCGGATATTTGGCTTATCCTT TGACGCAAAATCCACTTTGCTGTAA/C/TTGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8467a	70 A G	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAAACTGGGAAAACTCGGATATTTGGCTTATCCTT TG/A/GJCGCAAAATCCACTTTGCTGTAAACGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAGGAAAAATTACTG
8498	84 C T	AGGGTTACGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/C/TTAATACTTCATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCCCTAACTCAG

WI-18562	29	G A	CTAAGGAAAAATTAATGATGGAAATATC[G/A]ACAAATATTCACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTATCAGAAACGA
WI-18618	51	A C	ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCTTTTCGATGCAAAATATAATTGTAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T	TAAGTGTTCCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75	G A	GACTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTAAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAATACTACTACCTACTGCCAAACACACGGGCATCCACTCTGTCTTCAA TGCTCTTCCGTGAGAC
WI-18563	94	A G	AAATAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAGCCAAAGATATT
WI-18582b	69	T A	GTCTATTTCATTTAGCTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC TT[A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T C	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A G	AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44	G A	TTTATTACAATATTAGGTGGCACAATACTAACAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18715	76	G A	TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCCACCC
WI-18535	107	G A	GTAAATAAGTTTTATTGGCACAGCCAGCTCGTTTCATTCATATGCCATTGACATCTGCTGTGCCCT ACACAGGAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCCGTG
D17525	107	C T	AGAGTGGTGAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTAGTTCTGGCAGGTGAC TTCATCTCTTCGAACCTCAGTTTCTCATAAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAAC[CT TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGGTGGGCACCTCCTACGTCAAACATGAAGTG TGTTTCCCTTCAGTGCATCTGGGAAGATTCTACCTGACCAACAGTTCTTCAGCTTCCATTTCCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACCTGCCAACAGTTCACTTCATATATATAAAGCATTATTTT CTCTTTGAGGTGAATATAATTTATTTACAATG[GT]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAAGTAAACACAAATGAAGTGCATTATTCAA
DWU-447b	172	--- ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATAGTTTGTAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTGTAG GCTTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA[GT]ATCACTGTAAATTAATAGTTTGTAGAGCACAAAGCTTAGCTAAT CAACCATTATTTTCAATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTG TTAGGCTTCTTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAAAATTCAGTTTTTTCCAGTTCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGTGAG[CT]GAT AAATCAACTGTCCATCAGGTGAGGTGCTGCTCCATACCCAGCGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCATCACCATACAAAATTTA[A] A/TJGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131 A G	AAATCCAGGCATTTTCAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTCCACATTTATAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAACCTTGTGTTGAATATCCAGATGTTTGGTCT[AG] TGGTATGGCAGTGAGCAGGTATGTTTGTCTTTGCTTTCACAGTGAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATCAAGATGCTCCAGATGAAGATGCCGAG
DWU-525	97 A C	AACTGCATATAGATAATTATCCAGGATGTGTGGCTATTCTTTTCAAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T	CATTTCTTTGTAAAGGTAATGGACTCACAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTGTTCCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGTGTTTTACTTCTGATAGCCGGTGATTTCCCTCCTAGCAGACATG CCACACCGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C	CTTGATCATGGGTGGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T	CACACTGGCATCTAGGCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTGGAGAA[C/T]G CTGGTTCCCGAGCCACACCCGCTTTGACCCACACAGGCTGTTGAGGCAGGAGTGGTAAAGACGT AGCTGTAGACCCAAAGCAACACAGCCCTGGGACCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCAATCCCATCAATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A	TTCCAATGTAAGAGTCAAGTACCAAGTTAAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C	TTCCAATGTAAGAGTCAAGTACCAAGT[C/A]AACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T	TGTAAGGTGACTTCTATAAGCTTCTAAACTGCTAAACTTTCAATTTACTGAGATTATTTACGGCCAAT GTGTC[T/G]TGGGTCTGAGATTTGATTATCAGCTGGGTAAGTTAACCTGTTCCTGTTTCA

WI-18063	105	G A ---	---	AGGCTTTAAACTGATAACAAATTTGCCITTTAATCACAATACAAAACTCTGCACITTCATTCCTCCTTC
WI-18078	86	A T ---	---	CCATGTTTCTGATTTTGATGTAACTTAAAATTTGTG[A/T]CCTTTAACAATATACTGTAGCTGCA
WI-18091	90	T C ---	---	AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGTGAAGTGAAGTTCAGATTCAGAACTGGTCCAGTGTG
WI-18119	38	T C ---	---	TTGTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18142	66	T G ---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18178	68	T C ---	---	TTTCATCTCTAGAAGTTGACTT[C]GGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18244	35	G T ---	---	GCAATCTGAACAGTTTTGGTAGTGGTATTACAGAGGAT[C]TTGTAAATGGATTGGAGTACTTAC
WI-18245	115	G A ---	---	CACTATTTTCATCTGCTGAAATAGTTCACTAACCAACTACTGACAACAGITTAATTTTGGTTCTT
WI-18261	26	G A ---	---	TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCACCTTTTAAATCGAAAAATAATCTATATAC
WI-18268	88	C T ---	---	T[G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA
WI-18299f	107	C A ---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCTGGAGGTTAGTCTGGGG
WI-18299e	101	A G ---	---	GT[C]CGGCGGGATGGACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18299d	77	G A ---	---	TCAATCTGAAAACTTGTCTAAGCCAGCATGGGGT[G]TGGGAGGTGATTATGGCTGGGGAAGATG
WI-18299c	67	T G ---	---	GGCACTACCCGACAGCAGCATCTAGCACCACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
				ACAGATGTCAGTTGTTGAAATTGGCCCATTAAGTATGGGGCTTTCTTGTAAAGTCATCCAAA
				AGGCTTGGCAAGAGTTTGTCTATACACGGAGGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT
				GACAGAAGGTGGGCTGTC
				GATTTGAAGGAGTTCCTTTATTAAAC[G/A]TGAAAAGCGTGATAGAGGAAGTGTAAAGATAACAA
				CTTATAAATCTCCCAATTGTAGAAGTGAAAGATTG
				TAGGAGGGAAAAAGGAGGTGGGCTGCCTGGGCCCTCAAGACATGAGAAACGGGTGGTCTTCCAAGC
				TTCTTACTTCCCCCATAGAT[C]TCTGACAATGTGCTGCAGAAAGCCTCCAAACCTGGAAC
				TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACCTGGTTGCCAATTTTTT
				ATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAAATTCCTTTTGGCAATATTGACATATTCTG
				CAG
				TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACCTGGTTGCCAATTTTTT
				ATCTATTTG[G/A]GTCTGAGAAATCCACAATTTTGAAGAAATTCCTTTTGGCAATATTGACATATTCTG
				CAG
				TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACCTGGTTGCCAATTTTTT
				T/GATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAAATTCCTTTTGGCAATATTGACATATTCTG
				CAG

WI-18298b	52	G A ---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAATTG[G/A]TTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATGACATATTCTG CAG
WI-18299a	48	C T ---	---	TCACAAGTCAATCTCCATCCAAATGACAGTTTGTCTAAGATCATTAAT[A/C]TTTGGTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATTAATGACATATTCTG CAG
WI-18307	76	G A ---	---	TCAACTGTACCAAGTTAGCAGCAAGAGGATACCTCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAGCATCCAGATGGTTTATTGTAATCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---	---	TTGGTATGAATCTTTCTCTGACATTTACCAATCATCATTAACTCCGGGGGGTGGGTACTGATT TAT[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C ---	---	ATGAAAGTCACTTCAATCATAAGGGTCAAGAGAAAGAAATGTTTTCAGAT[T/C]TAAATCTATGAAAA GGTGTATCTGCTTGCATTTAAGAAACACACAAAGTCA
WI-18395	77	G C ---	---	TCTTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTTCTCGAAAAATTTGAAGAATAAAATTG ATTATTCAAG[G/C]TGCAATTGGTTTATACATATCTCTCTCTTAAATGCAAAAGCTATG
WI-18398	62	G T ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAGAAACAACTCAAGGGT[G/T] GATAACATTGCCAGTATAACCATAATTCAAACAAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A ---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCTTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAAT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18409a	20	C A ---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCAAGTGCTA
WI-18442	62	C T ---	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGACAGAGAGGAAACAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGAAACACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18452	38	G A ---	---	TTGATGTTAATACTGTCAITCTGGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAAACA
WI-18489	102	A C ---	---	ATATAAGCTGGAGACTGTGGAGGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAAACA[A/C]GGTTATGGCAATAGAGGGTGAAGAAAA AGGCCATATAAA
EST5b	93	A ---	---	CTGGTGGGAGGAAACAAATTGTGGTATATTCAATGAAAACTCTTCAGAAATAAGAAAGGAA CAAACTGAATCACACAACATGGACAAATCTCAAATCATTAATGCTGATGGAAAGAACCATTC TAAGAATACACAGTACAT

EST5	93 A ...	---	CTGGTGGGAGGAAACAAATGTGGTATATTCATACAAATGGAACACTCTTCAGAAATAAGAAAGGAA CAAACCACTGAATCACACAACATGGACAATCTCAAATCATATGCTGATGGAAGAAACCACTTCA TAAGAATACACAGTACAT
EST6	48 C ...	---	TTAGCTACTTTTCAGAAATGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTCTCTCTTTGCAACAAGACAAAAGCAACATTTTGCAATAGACAGAT
EST8	158 A ...	---	GGACAGGACCTCTATTCCCGCTGTGACAGCGGCTGATGAGTGGGCCCCAGGGATACCTGGGOC CTCTCTCAGGGCGCTCCAGGACCCAGAGCTGTCTCTGTTGAGTTTCCCTAGAGCTGTGCGGGCCA GATAGCTGTTCCCTGAGTTGCAAGCACGATGGAGATTGGACACTGTGTCTTTTGGTGGGT
WI-18740c	104 GT ...	---	TCCTCATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATCCAGTAGTG/GATAAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 C G ...	---	TCCTCATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCATTTACCATCATGTATC/GIAGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 CT ...	---	CCAAAGTCTCCTGTTGCTCATAAAGAAGTTTTGGGATGGGAGAGATCCAGACCCTTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACAA/C/TGATTCCAAACACAAAACCCCTTCCCC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCAATTTGTGTTTCTCTT TGAAGCAATGACAAGCACCTTACTTTCACGGTGGTTTTGTTTTCTTAT
WI-18746	114 GA ...	---	GCCAGCAGCTGAAGTCTTTTTCTCTCCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGTAATATTCTTG/AJTCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112	212 GA ...	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACAGATCAGTAGTGTCTATCTCATGACAACCCACAGAAACCGACGACAAA TCCTTTGCGAGATTTCTCTAGTGGCTTAGAACATGGCTTTTGAACAACCGGTGATATCTTTGAG GGTGACAAGGC/GA/TCTCTTCAAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ...	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTATAGAAGGCTATTTAGATCATGT CTCAATGGAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTTC/A/CATGATTAGCCGTGTAAC
WI-19057i	175 GA ...	---	CCCATTATTATAGCCAGTGTCTCAAAGAGTAGAGGAGGTCTACTGGTCTTTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACCGTGACAGCGGAAGTGGTATTGACGTCCAGGCACCGCAGCCACTG TCITCATGCAAGGAACACAGTGCCAGATCCCCACAGCTC/G/AJCTCTTCATCTTGGTTTGGCCACA

WI-20103	168 C T ...				TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCAATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA/C/TJTTCACTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ...				GCCTTACCCATTTGCACATATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAGGACAAGAAATGGA[G/A]JTGAATAAGTAGCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCCAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ...				TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAATAAACAATGCAATTTTAA/GJACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ...				GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAGTTGGA[G/A]JAAAGGGAGTTTCCACGCAGCCAGTGTGAGC TGC
WI-20613b	156 A C ...				GTCTCAAGGGGGAGAAAACCTGGTTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGCAGTTAGAAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAGTTGGA[G/A]JAGTTGAAAAAAGGGAGTTTCCACGCAGCCAGTGTGAGC TGC
WI-19984	47 A G ...				CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA/GJITATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCACACACTGGAATAAGGAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ...				GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAGTTTGACAG T/CJTGAAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTGTCTTCAATAGGAATCCATG TTATTTCTTCTTGGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ...				GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCTT[G/A]JAAAGTGGGAGCGT GGGCTCAGCAGGCTGTGCACCTCCCATCCCGTAAGACCTCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ...				AGCAGTGGCCTTATTGCATCCCAAAACACGCCTCTTGACCAGGCTGCCTCCTTGTGGCAGCAACGGC ACAGCTAATCTACTACAGTGTCTTTTAAAGTGAATAAGTGCAGAAAGAGGCACCG[G/A]JGGAAGCCG TCCTGGCGCTGGCAGTCCGTGGGACGGGATGGTTCTGCTGTTTGAATCTCAAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGCCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGT[C/C]CATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCATCATTACTGTTAAAGCCTCATTGTAATGTGTAATTCATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTTCACGCCCTGAGGCAATTAGACACTTTGGAAGATGCCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGGCTCTAAATTCACAGTGCTCTTTTCTCCTCACTGTATCCAGGTTCCCTCCAGAG GAGCCACCAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA[G/G]TGACGATGATGTGA[G/G]TATTAGAATG TACCATATTTTTTGTAAATATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTGTGGGTCAACCGTACAATGGTGTGGGA[G/G]TGACGATGATGTGAATATTAGAATG TACCATATTTTTTGTAAATATTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTT GGGAACAGAGAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATAGTATTTGGTCTTGGTGTGTGATGAAATCTGAG GCC[T/C]TGATTTAAATCTTTCATTGTATTGTGATTTCCTTTAGGTATATTGGCGTAAGTGAACCTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACCTTTTGCCAATGT[C/η]ATCGGGTTTGGTTT TCTTGATTATTAAACGGTTGTGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAAAATGGGGTCTGCTGCTACCTTGACCTTCCCTTCTCTGCTTCTCTCTCTCATCA TCATTCCCAACAACATCCTCTGCCA[C/η]ACACAACAAAACGTAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCACC GGCCCCCGGAGTGCAGTCCAGCGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGAGC AGCAAGGCCCTTCTCACTGGGTTGGTCAAAAG[G/A]TAGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCCGAGTCAACAGGACGGCTGTCTGGCCACAGACAGGGGCTGCCCTGTGGAGCCTGCCACC GGCCCCCGGAGTGCAGTCCAGCGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCACTGCGGGAGC ACCAGCAAGGCCCTTCTCACTGGGTTGGTCAAAAGTAGTACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAACCCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGCTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCGAGAAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAGAAAT[7] GACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCG/GC/AGAAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATCCCTCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTC[G/GGAGAAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTGTCACTGCCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCC[G/GCTGGCTG TGCACATTCCCTCTGCTCCAGAGACTGCCTCCGCCATCCACAGATGATGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCGGAGAAATGTTGTGAGGGGTTATTTTTTAATAGTGTTCATAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAAAGTGGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCAACTTAAAGACAGTGGATCATGAAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCCTCTATTATTTAAT[7]CTGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTTACACACCTACTAAAAAGTTATTATGAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAAACCC AAATGGCTAGAAC/G/GTGTAAATTAATTAATTTCAAAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTCAATTTCTTCTTCTTCTTAAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGATTGTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTATTATGCCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTAAATGCCACAAGACATAATTTA AAATAAATAAATTTGGGAAAGGTGTA[G/GA/ACAGTAGCCCCCATCAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTCGAAAGAAATTGCTCTGAAGCTTGTA TCTGATATCAGCAGGATTGTAGAACTTGTGCTGATTTTGACCTGTATTCAAGTTAACTGTTCCC CTTGGTATTGTTTAATACCTGTACATATCTTTGAGTTCAAC[G/GTCTTTAGTACGTGTGGCTTGTC CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAGACAAAGTCTGTGGCTTG

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WI-19042	193 A C ---	---	TTTGTCAAGTGTGGCTCTCGCAATGCCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAGAGTCCAAACAG ACACAATTTATACTCGGACAGAACTTCAGCATTTGTAATATGTAATAAATCTAACCATAACCA[AC]GGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	ATTGGCCCTGTACAGTTTGCTTATTATAAAATTCATTAACAACTACAGGTGTGAATGGTTAAAA TGTAAGCCCTCCAGTTCAATTTTCAGTTATTTCTGAGTGCAGACAGCTATTTTCGCACTGTATTAAAT GTAACCTATTATGAATAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[AC]ATAAAATGCTAAATGTCAATTTATCACTGGCATGTTTGACT
WI-18851	90 T A ---	---	GCTTCAATTGGCGATTGATTCAAGTCCCAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCCTTATTGATTCT[TA]GTAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[CG]GGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[CT]AGAGGCTGGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACTTCGTGTCTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	ACTCCTCTGCTGCTGCCAT[CG]ACTGTCCCTTTGAACCAGGAAAAGTACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTCTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTGCTGAGGACGTGGCATCTCTACTTACGTACGTGGGCATAAC ACATCGTGTAGGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTCTG
WI-18908	70 G C ---	---	TGGAAATCCCTTCACTCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[CG]TTAGGGAAACATTCCATCCCTTGAGTCAAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[AG]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGTGG
WI-19037a	47 C A ---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTCTAGCCACG[CA]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGTGG
WI-19054	66 T C ---	---	TTGAGGAGGTGGGTGAATGCTCTCTTGGCAGGATTTGTGACACTGCATTGCTGGGCTGTGTTC[CT] CJCGGCTCTTCTGGACCTTGACCGGTGGATACCGGCCATGTGCCATGGTATTGGGTCTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112	A	G	---	AGCCTGTGGCTTATGTCACCCACACAGAGGGTCTGTGAAAGTCTGGCTGCTGGATGGCCCTGCCC CCCTCTGGAAGGCTCTGACAGATGACTGGCTGGGAGGACGAG/GJTGCTTCTGGCCATCGGACATGGAAGC TCATTGCAAGTTGTTCTGAACACTGAGGCTTCTGTGTGGCCACCAGGCACCTACGGCTTCTCTCTCC AGATGTGCTTTGCCTGAGCAGACAGATCAGCATGGAATGCTCTTGGCCA
WI-19016b	184	C	A	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCAATTCACCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAAATGTGATTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCT CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCTCTCAA/CJA/CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGTGGGGTTTGCTTGTGCACTGTAG
WI-19016a	161	C	T	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCAATTCACCTGTTTTAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTTGTAAATGTGATTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTCT CTGAAACCTTAGATACATAGCCGAC/CJTGTATACAGAGGTTCTCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGTGGGGTTTGCTTGTGCACTGTAG
WI-20096	21	T	C	---	GGTTTTGGGGCATTTATTC/T/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCCC ACCCTCATCTAGAAACAATCTCTCTCGCCAGACTTG
WI-19591b	156	C	A	---	TGGGGCAATTTTAAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTATAAGATTAAAGGCAGTTACTTTATTTGAACAAAGGAAGTGCCATAAGCAACTCAGTGTGTGCC CTTAGGGTGGGAGCTCTCC/CJA/CTACCACCTCCCACCCCAAGGCATCATTTTGGAGAAAAA GTGCTTCTATCGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45	T	A	---	TGGGGCAATTTTAAACAAACCAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGGCAGTTACTTTATTTGAACAAAGGAAGTGCCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTCCCTACCACCTCCACACCCCAAGGCATCATTTTGGAGAAAAA GTGCTTCTATCGGCTAGCTGTGTTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125	G	A	---	TCCTCCAGCTCTGTCACTCTGTGCTTGAGGGTCTGTGTTACAGGCCCTCCAGGCATGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGACCCAGCTCTCTAGAGGCTCCA/GAJTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224	G	A	---	CTCTCCCTTAAGGAGCCTTGGCTTGCAGCCCCATTACAGAGGGATGGAAGTCAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCTGCTCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGAAC GGAAGGAAGGGGGCGGTCA/TG/AGGTGATGGCTTCTGGCTCTGGCTT
WI-19359a	39	T	C	---	GACGTGGACAAAGGAGTTTAAATGAATACTTTGTGTTG/T/CJCATGTTCAAAAAAGAGTATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACCTTAGTTTAATAATAA GGCTATTTGTCCACCACTCTTCGGGCAATGCTGCAATATCTCGGCTCAAGTGGAGGCCACGTG GGAACAAGGCCTCAGAAAAACAAAGGACATGCAGCCTCCCTGAGGCCAGTTCTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCTA/GGACAAACAGAAAGAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTCGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCAACCCTCCTCTACCAACCAAGCTCTCCGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAGCTGATGCAGCAGCATCCTTTCTGTGGTGGGAGGGCAGGAGATGAACCATAGGAGCCAAAAGTCAGACAAACAGAAAGGCACACCAAGCCTGAAACCCCTC CGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTCGAGGTTCTGACCCATGAGAGGCCCCCTC ACCCTCCTTCAACCCTCCTCTACCAACCAAGCTCTCCGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTTGGCTTTCATTTGTGGATTGGAAAAACACATTGGAAGAGGGACTTTCTCTGCAA AACCTTAAGAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTTGGCTTTCATTTGTGCGATTGGAAAAACCACTTGGAAAGAGGGACTT/GJTCCTG CAAAACCTTAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCACGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGCACACCTTGATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGATGATGTTGGCTCACACGTAACCAACACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGA/C/GITTCAGAGTAACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTCATGGTCTTAATTGAAGTGTATGTACTTTCTTTTGAATATCCTTTT TTCAATTAATAAT/CJCTAAACCACTCTATGTGTTCAACCTTCTGTTTAACTAAGATATGGGT TTTTGGAAAGGCCACAAAGTCACCACTCCATGAAGTGGCGAATGGTCTTGTGTTTGGAAAGCTCTC CAGGGTGTCTCCAGAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATCTCTTCT/CJTAAAAATATAATTTTCTCTTCTGCTCTTCCAA GTAAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATATAACACTACCTAGGGGGG TTTTCTCTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAGGCTGTGAGACATTGTAATAAGTCTTAGGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGCTCTGCGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTGATGC ATCCCCCATGCATTGGTTTGG/CJATGCTCCAGTGAGGCTTTGGGCAAGTCT

WI-20113	60 T C ---	---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTAGTGAATGAGCAAGACCTGAAATACTGTC/GGA AACAGTAAAGCAAATACCACACAATAGGAGGAATATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAATCTATTCCATAAACCCAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTATT
WI-20895	107 G C ---	---	---	TGATGGCAAAGTACAAGGCTCTGAAAGAACAGAGTAACAAAGAGCAGCGAGTGCAGCGTGTGGC CACTCCACCAGGCGAACACTTGACTTCATTAAAGGCAA/GC/CTTTACTCTGTACTTTTCCCTC CCACATAGTTTAAOCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72 T C ---	---	---	CCTGCAATCACAAAAGTGAACCTAGTTGATATTTTGAATCATACTTGATTAAACCACCTTCAGAAA TTCTAT/CJ/AAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161 A G ---	---	---	CTGGATTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGCAGATTCCCTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAA GTCATGAGACCTTAGCTGATCTCAT/GAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103 C T ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGCGGGTGA/C/TGCTCTTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAACCTGCTCTGCTGTAGAAGCTTCTCC
WI-19348b	98 G A ---	---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGCGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/GA/GTACGCTCTTCTCCAGGCTCATATGGATGTCTT CGAGTTGCACAGGGAACCTGCTCTGCTGTAGAAGCTTCTCC
WI-19635	98 A T ---	---	---	ATTAGTTCGTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACAATG TTAAAGGTACAGTAAATAACAGTATTAT/TATCTTATTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAGAACTTTGCTT T
WI-19641a	46 A G ---	---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/GJ/TATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52 C A ---	---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJA/GGGTAAACCAG GACTATTGCATGAGCATTCCTTAATACGTATTTTGTATGGACACAAAGTTTTCATGCTATTA
WI-19673b	180 C T ---	---	---	TCTGCCATGATCACAATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCAATTGCCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCAGCTGTAAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAACAATTTTTC/C/TCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAACACAGCCC

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WI-19873a	35 G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACCTTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTGCATCACCACCTGTAATCTAAT AGTGAAAGGGCAAATGATGTCAGTATCACTGTGAACAATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAACACAGCCC
WI-19724	35 A G ---	---	TTATTGGGAAACAAAGGATTGTAATTTGGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196 T C ---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTTGCCCTTCATGAGAAATGGTGGCTGGGATGGAGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAGAAACAGGCAATGTATCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGCCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85 A T ---	---	CTTCCCTCATCCCTCTTCACCACACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGTC[A/T]TTGGGTAGCAATGTGGAACACCACAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGAGGGGCTTATTGAGGGCCTTTGCCACTTGCTCATAGGCGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCAATTTCCCGGGCGTAGGCA
WI-19946	122 C T ---	---	CAATGGACTGAATGAGTGCCTGCTGGTGGGTGGGGGACACACACACCTTCAATACACGTCAAGGTGG CTTCCAGTTTGTAGAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT[C/T]TCTTCCCTG ACCCAGCGCACTCAGGAGCCAGTCTGTTTCAAAAAGTCAATTAACCTGCCAGAGAGTTTAC CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141 G A ---	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTAGGCCAAGGTTTGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAAGCAGCCACGTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40 G A ---	---	TTGGTTGGATACTTGTCTGAAAAAAGCAGTTTAAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAGATTTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCCCTATCCAAATCTATCTGCGTCTCTGAAAAACTGCAGA AAGGCATTGAAAGCTGTTCTTTAAGATATGGGATTCTTTTATCTT
WI-20218	26 T C ---	---	CCACACACTCTGGTTTTATAAGCTA[T/C]JAGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAAAACAATAAAATTGGAGGGGAACAGTGGGATGCAGAAAGATGACAACAGCCACATGTGCCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154 T G ---	---	CAACCTTTTGTACAAGGGACGTGAATTTCTGATGAAAGTTATCTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAATATCTCAGGCTTGATTGGGAGGGGCTGGGCTACCCCTTTCTCTTTTCCA TCCAGTCTATTGCCAGAT[G/C]CCAGAGAAAGCGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGGCTTACCTTCTGTGCTGACTCTCTCATGCTGGGACTTGTCTTTTGGGG

WI-20361a	192 G A ...	---		CTGGGAGTGCTGACCTAAGTGACATTTTTTTTTATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAAATATGGAATCTGATGTCGAGAGTTACACTCTGCACTCCAAAGCTA CAACAGTGCCACAGCTGAGAGGTTCCCTATACTTCTACTACTGTGACAATTTAGCG/AJATCCTTC AAATGGGAAAATTCCTAACTACAGAGACAATGGTCTCTACAGTAGGCCCG
WI-20572	75 A G ...	---		GAGCCAAACCCAAACAAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATTJA/GJTCATAAACATCATCTTTTACAACATGGAGAGCGAGGTAGGCCATAATTGTTCA AATTCATCTTCTCAAATTTTAAATTTGTTTAAATCCCAAAGGTGCCTATTGAATTTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ...	---		CATGACAAAAGACAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTTCTTAAGTACAAAATGCTAAACI G/AJGGAGCCGAGCTCTCCGCATTGAGG
WI-20593	79 A G ...	---		TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAGI/GJTTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCCTCACCAGACTAT CCAGAAGCCATCCATGGGATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ...	---		TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCCTCAI/CJATGTATCT TGTCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACCTTTTAAAGTTTGTGTTCTTTCTCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACCTGAGC AAAAGGCCACGTTGGGATAAAATCACTACCATCGACGCCACCAGTATT
WI-19066i	239 A G ...	---		TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAATCCTCAGTTCAGTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCCTGTAGTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGGCAAACTTTTCTTAAACGCCCTTCAGT/A/GJTTCTTTTA
WI-19066g	184 C T ...	---		TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAATCCTCAGTTCAGTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCCTGTAGTGAATTAATCTCTCCATATTCI/CJ/JGGATGCTCAATTAC AGTACCATTCAGGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTA
WI-19066f	148 T C ...	---		TGACAAAGGGAGAGAGGGAATTTCTACTATTGCAAGGAATCCTCAGTTCAGTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGGTGGTCAACCCTGTAGTGAATTAATCTCTCCATATTCI/CJ/JGGATGCTCAATTAC AGTACCATTCAGGGCAAACTTTTCTTAAACGCCCTTCAGTATTCTTTTA

WI-19066e	147 G C ---				TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTACCCAGTCCAAATCTCTACGAGGAACCTGG CATATGTTCTTGCG[G/C]TTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066c	100 G A ---				TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATC[G/A]TCTTACGAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066b	87 C T ---				TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTCAGCTGATCGTCTTACGAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-19066a	72 C T ---				TGACAAGGGAGAGAAGGGAAATTCTACTCATTGCAAGGAAATCCTCAGCTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTCAGCTGATCGTCTTACGAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGGCCTTCAGTAGTTCTTTTAA
WI-20660	105 G C ---				TTTACAGCGAGTTTTCCTGCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATAATGTG TGCTAAATAAATCTCCCTTTTGAATGATATTTG[G/C]TTAATAAGGGAAGCATTAATAATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACA AAGCTATCCACCCGCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120 C T ---				CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGTCTCCTGGCAGCCCTCCCTCAGTCTTCC TCCACCCGCTCTTCCCTCCAGCCCTGCCATGCATGTGCACCCCTGGT[C/T]TTGCGTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37 A G ---				TTCCCCAGGGTCTGTATTGCAGCTAAGCTCAAATG[T/A]GTTATTAACTTCTAGTTGCTTCTTGTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAAAATCAGACACAATAGAGAAGCCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACCTGCCCCCTTTAAATGGCATGACAAGGTGTC AGTGGCCCATCCAGCATGTGTGTCTATCTTGCACTACCTGCTCC
WI-18790	49 A T ---				GAAAGCCAGAGATTAGCCCCGATTCGGCATCTGTCAACAGGACAGAA/TJGCATGGACAAGGGA TGAGCTTTACAAGATGATGCACITTTGGAGATCAGAAAAATTCATATTTAAGCAAAGTGATACAAACA CAGTGATTTGGGAATGCOCT
WI-18987	35 G A ---				AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCCT[G/A]GTGGCCCAAGCCAGACACTCACCCACCTT CCCCAGTGCCCCGTGGATCTGTGCTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGCTGTCACAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA

WI-18919	26 C T ...			TGGATGAAACCACAGGGATTCCGGAC/TTGCCAGACCCCATTTTATACTTACATTTTCTCTACAGTG TTGTTTTGTGTTGTTGTTTTATTTTTTATACTTTGGCCATACCAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ...			CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ...			CTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ...			CTTCTGGTCAAGGCTTGGACAT/CTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ...			TCAGAAGCAGACATGGCATCTGTTCCCTGCTGCTGTTGGTTGTACCTTTACAGAGACCTGAATT TTAGAATTGCCAGTGTGCCAGAGTGAGTGAGTAAATCTCCTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCATAAACATATCAACCA[G/A]TAGCATTAAACCATTTTATTCCTGTCCTT AGTGTCTGAAGATGCTCACCAGTTTTCTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ...			CCAAGTTGCATCCATGTTGATTTCTGATGAGACTAGAGTGACAGT/AJGTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATATGCAAGATGCCCTATGGAATAATGCAGCTGC ATAATTAAACATATCAAGTCTCTTACAAATTTATTTCCGACGATGTCAGCTAAGTAGACCCCA ATGGGAGAGAAAAATGCCGTCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ...			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAGAACACACATTGGATG GCAGCATGGTTCTTCCCATTTATGGGCATGAAATATGTGTTTGAATAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTCTAAGAGGCTTTTGTGCTGAGTCAAGCAACACACTTGCCTGCTGCCCC CTTGGAG[G/C]TGGCATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ...			TTGAAATCCCAGTCTCTGGCCCCCAGGCAGGTCTGTCCACATAGATGTCTTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTCTTGATTCTGAACTGGAAACTGAACCAAGTTTGCCTTTCTCCTAGTCACC AAGCATACTT/CJTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ...			GTCTCCCCAGAGTCTCTGCACCCCCAGCCCCCTGTCTGCTGTAGGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGGCCCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACCAGGGGGCCATCCTTCTCAATACAGCCQ[T/C]G CCCTTGCAGTCCCTATTTCAAAATAAAATAGTGTCTCTTGCCTGTCTGT
WI-19135	20 G A ...			CAGTTACCTGCTTTGCCTC[G/A]AAAGTGTCAATTTGTAAATTTAGTATTAACCTGTGTAAAGT GTCTGTAGGTACGTTTTATATATAAGGACAGACCAAAAAATCAACCTATCAAGCTTCAAAAACT TTGGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54 G A	TACACAGAGGTCGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGAAAGG[A]GATGGAGAC CTGCTCCCAAGCTCTTCTGTGACGCCGTTTACATGGGAACAGGGTTAATCTGTGTAGGGAGGT CACCTTACCCCTTTTTCATAGGGGAAGAGTGTACACTCTGCTGCTATCTCAGGGGAATGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222 G C	GTGCCAGTCTTCCAGAAAGCAAGACTGCCCTTCATTCAGCCTTCTGACCTCCAGCCTTCTAAGG CTCAGCCCCAAGGACTCTGTGGCTGCCAGCTTGTAGCTATCTATCTATATTCATTTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G]CTGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110 C A	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGGTTGGCAGACAACACTAG[C]AATTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66 C T	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGATTTACACGAGGGTAGA[C]TGGCAGATGCCTGACAGAGAGTGGTGGCAGACAACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGGTCTCTGTGTGAAGCCACCGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112 T C	GGCTGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAGGGTGCCCT CATCCAGCAACCTGTCCCTTGTGGGTGATGATCACTGTGCTGTG[C]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173 A G	TTCAGGAGGTGGAGTTCGTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTGTGATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATGTTTCAAAATGGTGGAA[A]GJGCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCACACTA
WI-19222	179 C T	CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGCCTCTATGTTTCTGTAGGTAGTGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGACTCTGCGGAAC[C]TJTTTACACCTCTTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGTACACTGACGTGTCCAGAAAGCAGACTTT
WI-19117	134 A G	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCCTAAGACAAGAACATTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAACACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A]GJTAGCTATTTTTTCCTAAGACATTTTTCATTCATGAATTTTCAAGTTTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263 C T ---		CTCCTGTTCTGTGACCTGACAGGGTGACACAGCCCTTTTACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGAGCAC TTATCCACTTTGCTCTCTCTACCTCGGCACCTGGGTGGGAAAGGG
WI-19134a	162 T C ---		CTCCTGTTCTGTGACCTGACAGGGTGACACAGCCCTTTTACACTCTGTCTCTCTATCTTCTCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGCAGCCAGGGTTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACCTATCTCTTTTCAGAG CACTTCATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGAA
WI-19224	112 C T ---		GGTTTCAACAGCTTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCATAATCCAGCAGGCCAGAAAGACTTCC AGGAAACTCATTCAGGAGGTGAAAATGATGATGACTCTCTCCAAGATGAAAA
WI-19201	179 T C ---		GCAGTCTTAAGGACCCTGGCCATTAGCTCTTGGCTTTTGATGGCATTCTTTCCACCCTTGTCTCTC CTTTGCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCAACACTTTGCCCTGCAGGTGCACCGGAAAGGAC/TCTGGGGGATAAAATTCAAAAAA GTGTGATGTCTGCTCAGAAAGGTCAGACTCCATGTCTGCCTTGGGCTCAA
WI-18034	45 T C ---		GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAAT/CJACTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGTGTTGAAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTGCAATTGAC ATTGCTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25 C G ---		TGTTCTGAGTCACGCTGAGGAG/CJCTTCACTCAGGAGTTCATCTGAGATGATCATGATGTTCA TGCGACGTATATTTCTTTGGAAACAGATGAAGCAGAGGAACTCTTAATACCTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAACTCTGTAGTTTGAACCTCAAGGGAGAAAGGTAT AGTGBAATGAGTGTGAGCATCGGGCTTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---		AAAGGAGGGAGAATCTTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGGAA/A/ GJAAAAAGCATCTNTCAAGCTTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---		AAAGGAGGGAGAATCTTTTTACATAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGG[G/A/A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---		GGCAGCAGCTTTTTTAATTTGAACACTTTCTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAAATTGCAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121 C T ---		CAGAGGGAAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCGCAGGACAGAGGGGGC/CJTGACAGCA GCGCATGCCACAAACATTCA

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WI-18017	87 C A	ACAAAGAAATGGAATAGGTTGCGAAACCTTATCTGTCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAAATTATATCTCTTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G	TTATTGCGTCTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTAGAAACCCNTCGATTCTGAATATCC[C/A]GTGGCGCATATGCAAGGAAGATGA
WI-18254	64 T C	TATACGGATCATGTATTTGTGTGACACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]GCCAAATTCCTCTTGCTTCTGTTAGTCAGTCTCTCCAAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A	CAATGGGTGGACTGAGTGAATAAACGCATATTGAGAACAAAGACGGCCTCTGGCCNCTCTGCGTCC AAGGCTGTAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACGGCTG[C/A]GTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40 C T	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTNCCTTAGCTTCATTCTCATAATGCCAAA
WI-18459b	64 T C	GGCAAGAGACAGAGATTTAATTGAATAAACTCCAGGCTGTGACACGGTGGGAGACACAAAT[/ C]GAGTAATTAACAACATAATTTTANATGACAGTGCATTAATTAACGTCCTGGGTAAGCCAGAG GGGAGGAGGGGCTTTCA
WI-22585	56 A G	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAGTGAACAAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G	GGCTGTGGAGTAACAGAACTTGATGGAAAATGG[C/A]GTTCTGTGTAGATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A	GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGAGCAACTCCTTTTGAACCTTTTAT TTTCTGGCAGGAAGA[G/A]GGATCCAGCAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98 C T	GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATGATG AAAATATTTGGAAGTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAGATATTAAATGCCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTGATTTTCCACCTCAATTAAGAAATGGAACATGT CTTATAATTGTAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T	TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAGA[C/T]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20501a	125 T C	TCAGAATTGCTTCCACTGCCCCCAACCAAGAAATTTAATGAATGNCNTTACAAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGCATGACAGGATTAGTCTCTCTGTTT[C]CTTGGT GCAAGTTTGAACCAAGTGAATTATGTACCAITGCATCAGAGCATCTGTTCCCTGTCAGATCCCCACTAG

WI-20561b	94 T C ---	---	CGTTGCTATTATAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTGTACTTCAGATGAAAAATCCTTACATGTC[G]GGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTTNCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---	---	CGTTGCTATTATAAGATGGCTGTTT[G]TAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTTCAGATAAAGAAATTTNCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---	---	GCCTTCATTTTCTGTCAACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAACATAT/AJATAAATCTATATATATATATACACACAAACACATCTACCAGCACTGTGAAGACACACAGACTAGGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCAGAGTTTGTCTCTATGCAA
WI-20116c	59 T A ---	---	GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20116b	59 T A ---	---	GCCTTCATTTTCTGTCAACCCACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTT/AJTAGAACATATATAAATCTATATATATATATACACACAAACACATCTACCAGCACTGTGAAGACACACAGACTAGGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCAGAGTTTGTCTCTATGCAA
WI-20116a	22 C G ---	---	GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	GCCTTCATTTTCTGTCAACCCAC[C]GCTGTCCACAGTTATGTTGGCCTTCAATATATGGCGTTAGAA
WI-20466a	133 G A ---	---	CATATATAAATCTATATATATATATACACACAAACACATCTACCAGCACTGTGAAGACACACAGACTAGGGCTTTACTAGGCTTGGGGCTCTCCCATGCCACTTAAATAATGNGCAGAGTTTGTCTCTATGCAA
WI-20466b	133 G A ---	---	GAAITTCACACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI-20466b	133 G A ---	---	AAAGATTGCAGTCCTGGGACACAGTTTGGAAAAACACTATTTATAAGTTGCACATATTACAAACAGNTCCCAAATGGTGAAACTGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[G/A]JGTGAACATAATGTTTAAAAAGTTAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAATACAGTAACACTACTTTTATTTCTGCTCTTTATCCCTTTTCAGGTTGATT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[G]AGTCTCTTTTATGGGGTATTTCA
WI-21034b	148 T C ---	---	GTTGTTAACAAAGTTAAAACTATTGGAACATACTTTGTAATTTTATTCGAGGAAGAAGAAATCTATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-22091c	205 G A ---	---	AGAAATGGACAATGATGCAGATGATTGTGAGCATTTTGTAGAGCAATTTGATGAGAAAGTGGTGATTAGAAGGATACAGCATAAATTTAAATTTGTAACATGCTTATCTAGCTAACCTAATCTGTTCTGTAGAATTAAGTGGTGGGAGATTGGATAGAT[C]GCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI-22091c	205 G A ---	---	GGCGTGTATTGATGCAATGTCCAAACCAAGTCAAGCTATCATGAAATCCAAATATTTCCCACTAGAGACATGCAGAGCAATGTCAATTAACATACAGCATATTACCTCCCCCTTAAGTGAAGTCAATAATTTCTATTGCTGTAGCTTTTAAAGGTTTAAAAATGTGTAGCATTAAGTGGTATTTACTTGAGGGCAACA[G/A]AATACGGCTTAAACACACACTAAATCATGAGGCTCAGGGATTG

WI-21805a	45 A T ---	---	CAACTGCTCTGAGGCTCTTCACTAGCTGATTTATAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGTGGATATGTTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGGCTTTTGTAGCTTAAGTCTGTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTGTAACCTTTTTTATTGAATTATTGAC TCTGCCCGGTGTCTGCTGCTTCAACTCCAGTCTGTCAATGCCCTGTAGGTGGGTCCCCAG GTCTGGGCTTCTGAGGTCTTCTGAGGTCTTCTGAGTGAAGGAGGCGAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCTCT CAAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGCAGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTTCAAGCCAAATTCACACTGGGAAAAACACACCCTCACAAAGATGCCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAAACATTTTTTA/CJAATTATCTA
WI-21449b	222 C T ---	---	AACAGCAGCAGTCACCTCCAAATGCAAAAAAATTACAAATTTTAGAATAAAATTATAATGTTTA TAATGGGGTTCAGAAAGANTTGAAGGTACAAAGATCAATACGCGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGTCCAAAGCTGACAAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTTCACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---	---	GCTTACAAAGGAAGCCTGTGGACAGGCGAGNTGGTGGAAACCGACTCCAGCTGGAAAAACCTGCCCTC CCATCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGAGTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCGGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAACCAACCAACCAACCAACCAACCA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCGGTGCTAGCAGAGCTCATGGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/C/AJAAAAACCAAAACCAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI-21808b	148 G A ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACACGTGCAGTCCGTTCAACAGCTGTAAA AACAAGCCCAACCCAAAGACATCACAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI-21609a	42 C T	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAAA[C/T]GTGCAGTCGTTTCAAGCTGT AAAAAAGCCCAAAACCAAGACATCAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTA AAGGATGTTTCAAAGGAGGTCGCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI-22512a	104 T G	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGGCAGGCAGCTACACTTGACTGCA
WI-21028b	139 A G	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGGATGTGACAGGGG TTTC/GJTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121 A C	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCGTGATTGATTGAGCAATCTAGGGGJAC/TATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58 A G	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/GJTTTCA TCATAAGACACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-18829b	35 T A	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTT/AJAATACTTATGTGTACTTCTTGATTCTCA TCATAAGACACAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGGAAGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A	CTCTGAACATAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCATI/AJACAT TGGCTGGAATGAGGTGTCAGGAAATAAANTGCACAAATCTAACCCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGGTAAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGGCCCTTAGGT
WI-22130b	165 C T	TGTTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTCCCTCTCCTGACAC CAGCAAGGGGGAGGCACCATCACGGGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGGAANAGACCCCGCGCTTGCTC/TGJTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAAGTCCCTGTGATGGGAATGAC

WI-21681	117 G C	GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTCACACAAAACCTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 T C	TCAGTTTAAACACATTATCAAGGAT/CJAGATTAAATTAATGTGAGGTGAGCATAAAAGGGAGATTATAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTTATTAAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G	TGCTTGATTAAATGGTGGTTTACATTATCCTATTTTCACAGATGGAACACAGAAAATACCAGCTTTTTAA[A/G]TAGCAATATCTATTATAATAATATTGAAATAACACCATAATAATATCATCTAAAGGAAGTAATCTAATGTGTTGATTTTCAGAGGGGAGAAAACATTACCTCTAGAGCTAGGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A	TTGCTATAATTTCTTAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGACAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACCTAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCACTGAACCTCACCCAGCTGAAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97 C T	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATCTTATAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAATGGACTATTTGCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 A C	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTACCCCGATGCTTCTCTGCAAAATGGACTATTTGCCAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 G T	TTACCTTCCAAACCCAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTAAATCAATAAGCCAAAGACAATAGGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACCCATCATCTGCCACAGAACC TTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTTGGACCTGAAGCTTCAGCATCCCTTCTTAGGG
WI-21703d	197 A G	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTGGGCGAGGGCTCTGCATCCCCCTTCTCAGCACAGCACCATCTTACCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTCCTTCTCACCAGGGTAAGAAATGCAGGTATTTCAGAGGGGAGTGAGTCTGGGA[A/G]GTGGGACAGCACAGCTAGGGGCAAGGACTTAAGGGAACITTTGGGGGAAGAG

WI-21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCGCAGGGCTC TGATCCCCCTTCTCAGCACAGCACCATTCTCACCCCTCCTGGGAAAGCAGCATTTGBAGCCCTACACC AGCTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCACAGCTAGGGCAAGGACTTAAGGGAACCTGTGGGGAAGAG
WI-22663c	139 G A ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCAGTGGTGCACCTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTTGTAATGTGGGT
WI-22663b	55 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCAGTGGTGCACCTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTTGTAATGTGGGT
WI-22663a	38 C T ---	---	CCCTTGTGAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTAGCCGGCGCTCGCTAATCTT TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCAGTGGTGCACCTTAC AGGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTGAAATCCGTTGTAATGTGGGT
WI-22668	99 A G ---	---	TCCTTTATCCTGCTGCTGCCTGAGTATCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACTTAACAAATAGTTTTCTGTAATATTGA/JTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI-22631a	52 T C ---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTTCGATJ/CJAGCACCATTTT CAAGTTTAGGCAAGTATTTAACCTCTCAGGCTCATTTCTCTTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAAATCAACTGAAATTTT
WI-20258	157 G T ---	---	AATCCACATTTCACGGAGGGGAGCCAGCTGCGCATGCTCCAGGCTCACAGCAGCGCGGCTAC TCTGCTGGTGGTTTGGTGCCAGGTGAGATGGTGACGGCGATTGGAACCCGTAAAGGCATGACAACG GGAGGCCGCGGGGTTCAG/GTGGGTTGACGAGGTGCATGGCTGGCAGCGGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTCCGGGGAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAAATCTAGGGTCT ACTAAATAATCTAGTACTTGTTCACCTCTCCTGCTAATCTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734b	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGCCCTG/AJCTTTAGAAGACATTACCCA AATGATGAGAGGCCAGCTCGTGAAGCCATAGTTTGGATGGCGAGACTTTTCGGCAGAGGAAAT AGCAAGTGCAAAGGGCTGAGGGAGAAATGAACCTTGGGCTTGTCTACAGGTTGAAAGGCGGCGCGT NTGGCTGAGGTTTAGTGATG

WI-22724	117	A G ---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTAGAGATATAGGA CAATCAAGATTGTCAAAATGTATAGTAAGCTGTTAAAGCTTCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48	G A ---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTACCAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI- 22775a	60	A G ---	---	TGCTGTTTCTTTAGTTTCATGACGTTTATCACAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCAATTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143	CT ---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---	---	TCTCTGCTGCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCACACACACCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAATTCGAAGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CTG[A/T]TGGCGTGGTATGTTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	CT ---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGTGTCCTCCCATTTGTCTCCACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTTACTAT GACTTTTCATTGATTTTATTTGTTTCTTCCATTCTCTGTCAAACCTTTTC[A/T]TTTGTATAA ACTGTTTCTAAACTTCACTTAATTCCTATCTGTATTNCTGTAGTCCCTGAACTTCTTTAGAGG
WI-21186	95	G A ---	---	AGCGAGCATCAGAAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTTAAGTGTTCAG ATGCTGCTTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATTCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI- 21187a	94	A G ---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAATAACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GNTCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	TTTCCCACATACCAATGCACCTGTTGTATAAATAATTCGTTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTAATAACAAATAATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTATTTTCCATGTATAAAAGCTT AACACA
WI-19937d	186 G A ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTCG/AJTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCAATGCTCAGGAAGAA
WI-19937c	185 C T ---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACCAATGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTCG/AJTCCAAACCTTC CAAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCAATGCTCAGGAAGAA
WI-21117b	227 C T ---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACCTGAAATCTGTTACAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACATTTTCAGAGCCCTTCAAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTACAGCTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTCTTCTACTGAATCTGGGTGGGAG
WI-21122a	42 C T ---	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATTCATCAIC/TJTTAACAGGAACCTCTGTTTTTCC TTATTCAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTTGTGGGTGCT
WI-21254	53 A G ---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTGGCGGAACTATTCACAGGAG/A/GJCAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	AAGGAAACTGCATGGGTACAAATG/TJCCAAATTCATACTTAACAAGGTGGGGAACGGGTCAATTCT TGGCTGCTCCAGAACAAAGGGCGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCT/CJATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGC/TJ GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGTCAAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37 T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAAGGTGGCACAATTTAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---	---	GTGACAAGAGGTGAAGCAAGGGGACAGGGGCAGGCGAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---	---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATT/CJCATTAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTGCTGATCATTGATAATGACAGATCCAACAT GAACTCCTGAAGCAATGAATATTTACCTTGCTTTCATGCAATTTAGGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACACAGATCTAAGGAATTGTGACAGGGATCTTCT
WI-21149a	167 G A ---	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCAC AAATAGTGGCTTTTTTTTTTAAACAATGACCTTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACAC[G/A]TGCTTCAGAAATCGGCGATTTGCACAAATGGTT TGGGGCAGGTTCTGTGTTAAACATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188 A G ---	---	GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTGATGAATTTGTTTTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCT GAACTGACACGCACTCATGTCTGCATGGGAACCTCTGSSGAGAAGACCT
WI-21382d	125 C G ---	---	CCATTGCAGTCCAGAGATGAGAACTGGACAGAGCAATCATGAACAGCGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGGGGTTTGGATCCAGTGGGATNGGCTTCC[C/G]AGGTT GCAACCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGTAATGGGAGCAGAGAGCTGCCATCCTC AGTCAGGTCCGAGTCCAGGTCAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201 G A ---	---	TCCCTGAGGTTGGAGTCTTAGCATAGTCCCTCCCTCAAGAGGGGCAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCAGGAACATGCCAGGCTGCTGTAATGGCAGGGTCACTTTACCAGGGC[G /A]CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---	---	CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCA[A/C]GTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---	---	CAAAATAGAAATTTCTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI- 21627b	153	A G ---	---	GCATGAAAGAAGTCCAAATCAGACITTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATAATTAAACCATAATTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21627a	106	A G ---	---	GCATGAAAGAAGTCCAAATCAGACITTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTC[A/G]TATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAAACCATAATTTACATAATTTGTAGG GACAGTACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI- 21399a	75	C T ---	---	GGATTGAGTCCCAACTTGATCTCAAAATTCATCTTGCATGTAACAAGCTCATCCCTCTAAAGTT TCAGTTT[C/T]TCCACAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCATTGTCTCTGAGGTTGTGTGCCCTAGGACTAGGTAGGATCTCTCTTGTCTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATACTTGT
WI- 20328a	68	G A ---	---	CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGGCCCTACT
WI-21249	155	T C ---	---	TTCTGGCATCAATGTACATGTAATCCAAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAAGAACATTATAAGGTAAT AAAACCTAGGTGTATACCTA[T/C]ATGGAACTAGTTTATTTCCNATTTAACTACTGTTTCAATGCGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTATAAAACATTGAGA
WI-21504	147	C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAAATTCAGTGGGGGCACGGCCGTTGGCTCCAGCTGGGTTTTCOC AGATGCAACAAT[C/T]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115	G A ---	---	CTGCACCGAGGAGCAGCTGCTGGCAGGGACTAATAAACCCCTTCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACAGCTTCAGACCCCTT
WI- 21475c	181	A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNGAGGCTGGGGTGAGCTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACGTGGCTCTTTGGAGAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTTCCCTCCCTGAAG

WI- 21475b	117 A T	TAGCCCTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGCTGCCAAACCCAGGCTTCTC/TCTGTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAAAGGCAAAAGCCACAGCAAC ACTTAGAGCAAGACCTTCCGTTCTCCACCCTATTTCCTCCCTGAAG
WI- 20893d	207 A G	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTACTAGGAATACAATCATTTGTACGTAAGTTTCATCCCGACTCC AGGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTCCTCTCTTTTACAATGCAGT TTC/A/GIACATAACATTTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 20893c	179 T C	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGTGCAGGG CTGTCTTCGGCGTTTAAAGTGTACTAGGAATACAATCATTTGTACGTAAGTTTCATCCCGACTCC AGGTCAGGCCAAACCTTTCGGTGGACCTGGGNAACCTGCCATTCCTCTCTTTTACAATGC AGTTCAACATAACATTTGGTAGAGTAAACAACAACCAAGCCTAAATG
WI- 19941c	71 C G	GAGCTCAAGGGAAGACCCCTTACCAGATAGGACTAACTGGAGGGTGGAAAGGAACAAGGTGAAA GGTATC/GJGGTCTGTGGAGACAAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTCCTATTCCAGTGCATGTCCCTTAAAT AAACTGGGTACAGGAGCATTTNGAAGAGGAGAACCAAGGACAGAAAGCAAGCG
WI- 21552b	166 C A	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATCGATCTCCTTCACCTCAAGCATTTATCCATAGTTTACAAAGAA TCCAAGTACTCTTGATTATTTAAAATGTA/C/AJAATTAATTTATTGAATTTAGTTACCCC ATTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI- 21552a	66 G A	TGGGTACATGGACAGATGTATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATCGATCTCCTTCACCTCAAGCATTTATCCATAGTTTACAAAG AATCCAAGTACTCTTGATTATTTAAAATGTACAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54 C G	TCCTGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTC/GITAGAGAGGA AAGAGCTGGTGCTGCTGTGGAGGAACGTCCAGGTCCGGGAAAGGCACCTGCTGCTGTGATCTGTC TCAGTGATGGAGGCTCCACTCGCCCCACAGGCAGCCTCGGGGCCAGAGATGAGATATGCTGTA TCCAGTACAGGGGCTGCTGGTGGGGTCCCCAACAGCTCCTCTTTGGGGG
WI- 21513b	192 G A	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACCTCTCTAAGGCGAGGACAAAGCAACTTCCATT ATTCTTAGTTTAGACCAGAACTCTTAATTTTATATTCTCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAAGATAAGAGGCAGTGTAA[G/AJAGTAG TATCTCTACATACCACAGTATACAATGATGCCCTTCTGCAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTGACCTCTCTTAGGACTGGTCATGAGCTGACAAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGCJC /JACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	---	TTGAACCTCTGAAGGTGGCTTATGTCTGACCTCTCTTAGGACTGGTCATGAGCTGACAAAGCATAG AGGCAAGTATCTCAACATTACAAACCCCAJ/GJCTTCAAGGAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	---	ATGAACATGTTGCAGTGGGATGAATC/GJTTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATTTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---	---	---	TTTCATCGGTTCTTAATACAGTACAATCCTTTTGTGAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAAATTAACATTG/JGJCTAGTTCAGTGATTAGT CACAGAANTTAACATCTGCCAGATGTACACAAATTTGGTAAAAACTACAGCTTCTCTCCACGGGA G
WI- 21695a	141 A C ---	---	---	ATACACAGGCCACAAATTCAGGATGGAAGGCGAGTGGGCACCTTGGAGTGACTACACATGGCAATA AGCAGCCTATCTCTTACCACACAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCTTTCCAA GGGAATA/JCJTACTACACTAAGCCTACACTGTACTGTGAGATCATGGTGAACAAAGGCCACAGGC AGTGGGAGGAATGTGATGACTTCACTGTGTTCAAGNTTCTAAGGCCACGAT
WI- 21574a	235 C T ---	---	---	AAACCCAGAAATTTAGGTACTTTTGATTTATGAGGAACCTCACTATAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTCCACTGATCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCTCTCTGCTCAGGTGGGA
WI- 21644c	151 T A ---	---	---	TGACTGCCAAGATTTAGGCCCCAACTTAGGAGCAAGGTCACCTTAACCTTTCAGGAAGCTTTGGGT GTGACCCACTGCATAAATGGATTTTACCATANTATTTAACAGACTCAAAGTGATACATACAAGCTTG TTTCATAAATAAGGGA/JTTCATCAAGATCCATGGAATGATGCAGTTTAAATGTGTTCTCAGC TTGCCTACTGACCACCTTCTCTTTTCTAAATATGGCAACAGCAGCAAGTC
WI- 21614b	55 G A ---	---	---	TGCTTTAACCTCAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC/GAJTTTTAACA AACCTCATATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGGAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTACATATTAAGATAAGGATGGACT CTTTCACTGAGTATTATC/JAGGACACAAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATCTATATTGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT[7A]GTC CTCCCTATGGGTACTGTGAATTTCAATAGGGTGTGGGATAGTACATGACAAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTTGGGAATTACAGGAACATAAAGGATATAATGAGTGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGGTTAAATTTGG
WI-21860	120 CT ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCTCTCCACTGCT TACTGTGTACCAAGAAAGGCAGAAAGCAGCTCACCCAGCCTAACCTGGCC[7T]GTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAACTGGGATGCAGGGAGAAAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 CT ---	---	TGGAAGTAGCCTCTCTGGACAGAAAGAATATTTGTGGTCCATGTGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTCCTT GTCTGTAGTTTCCAGGGCTGGCACAGAGGTGAGGCAGAAATNTGGGGTCCCAGTGGATCTCCCC ACAACTTC[7C]TTCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-19105a	33 TC ---	---	TGGAAGTAGCCTCTCTGGACAGAAAGAATATTT[7C]GTGGTCCATGTGGTGTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGGTCATAGACACGGGTGAGCTCATGGTGGAACTCCTC CTGTCTGTAGTTTCCAGGGCTGGGCACAGAGGTGAGGCAGAAATNTGGGGTCCCAGTGGATCTC CCACAACCTCTCTCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-21760c	81 CA ---	---	CAAACCTAGTCACTCTACTGATGCAATGATTGGAGGTGCTTCTCTAGCTTTACAATAAGNGGAGG GACCTTGACTGCA[7C]A[7C]CTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 AG ---	---	CAAACCTAGTCACTCTACTGATGCAATGATTGG[7G]A[7G]GGTGTCTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 TC ---	---	TCTGCCATATTGTTCCAGGACCACATACTACTGTTATTCTCTTTTGAGGAAAACCCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGGTAAAAATCCTTTTCCTTACCCAAAAGGA ACTTCTTAATCACCGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[7C] AGAGACAATTCAATGTTTCAATCTTTTTCAGGGTGTGCTTTACTTGGGGGGC
WI-20934a	72 TG ---	---	CCAACATGCAACATAGTCTTCACTTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[7G]TCTAAGACAAATGGTCAAAATATTCAAATGGCTGGCACTAGTGGTAAATTCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCAGGAGA
WI-21561	55 TG ---	---	TTTCCATTTTATTAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCT[7G]CCTCTTAAC CTCTCCAGGCAAGGAAAAAGTGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAAAAAGTGCTTATTAAAGTAAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTTGGATGCATTGTCCCCA

WI-21961c	200 T G	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACITTTATTT TTCCGTAAGTTATTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCGATTTGTGTGATT TTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCC/T/G/C TCCACATTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATG
WI-21961b	73 G A	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTATTATTATT TTCC/G/ATTAAGTTATTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCGATTTGTGTG ATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACTCGGTCTTTTATCCCTCGCCCCC TCCACATTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATG
WI-21956	26 T G	CCCACCTTGGGTCTCTTCAAGTGAAT/T/GTTCCTTCTGTTCTTAAAGCCTTTTAAATGAACCT TCCATTCTGTTCTGAACTTGCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATTTCTTTCTT CTGAGCGCGCAAGGACTGAAGTTGCTGTGACCTGTAGGGTTTCGACGCGGTAACTCAGGGTAACTC CTATCTCTTCCACCGGTAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A	CAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGAACTGTACTGTAAACAACATAT TTTTGTAGAAGCATGAGTGAGTGTGTGTGTGCGCGCGCGCGCATGGCACTGAGG GGATTGCAATGGG/G/AJACAGGATAAAAGGTATAAAACCTTGGTCCGAAATCTTTGCTTATTAAAC CTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAGAGAGGTAGA
WI-21930c	146 G C	TATACTGGTTTTGGTTACATGGATGAATGCTAATGGTGAAGTCTGAGATTTAGTGATCCCATCA CCTGAGTAGTGATGATGATCCCACTTGAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCAT TTTGAGTCT/G/C/CATAGTCCATTATACACTCTGTATGCCCTTTGCATACCCATAGCTTAACCTCCC
WI-21139a	165 T C	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAAATGGGTACAA TGTGGGTCAGCAGTAAAGGAACTAATACAT/T/C/GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217 G T	CACATGCAATGAAATACACAGGTAAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGC TGTTGGTTGCTTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGTACAA AATTTGTTCTCTCAGTCTTTCATTAAGTAAATTCATAAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA/G/TJATTAATAATTGCATATTTTGAGGCTACTCT
WI-22082e	179 G A	CAGGACTTGGTTGCTGTCCCACTGCACATAATGTCCCTTTTGTGAGTTATTGGTTGTGTGCG TTTTCTTTTGCATAAGAAATATGTCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGGAGG GTACACGGGGCTCCGCTCAGTCCCGCGGAGGACGTATT/C/G/ACTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAAATCCTCTTTGCTGTCAACCTCT

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WI-22082b	67 C T ---	---	CAGGACTGGTTTGTGTCOCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATGGTTGTGTG/C /TGTCTTCTTTTGCATAAGAAATATGTCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCGTCCGCTCAGTCCCGCGAAGGAGTATTGCGTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAATCTCTTTGTGTCGAACCTCT
WI-20993	139 A G ---	---	AACACAACTCCATGCTTTCAAGATCCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAACCCCTGG GCTTCTA/GTAAACAAGTGAATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGGCTATTTCAGGCTCTCCTAGTCTCATCCACACATCACC
WI-21723b	125 A G ---	---	AAGCGATTTTATTAATGATTTGGACATACTGTAGGTCAAATAATTTCTGAAGATAACAATA TGGACTTTAAAGCTCGACATAAAATAGTAGCTTCAAAGGGTTAGTCATATCCCA/G/CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	AAGCGATTTTATTAATGATTTGGACATACTGTAGGTCAAATAATTTCTGAAGATAACAATA TGGACTTTAAAGCTC/G/A/CATATAAATTAGTAGCTTCAAAGGGTTAGTCATATCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99 T G ---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTT/G/CCCCATTTCTCTAATCTCTTTGCCTTACAA TATATTACCTTGTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACACATGTGCACACAC/G/AGAGGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAAGTGCAAAAAGGCTTCATTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	CTGAGGCTGCTCTAACTTCAATNTGACGGAGCGAGTTTCTGGCTTGGAAATAACTGAAAGATTCA TTTCTCTTTGTGTACAAAGGATTCAAATAATTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CTC/G/CAATACACACCACCAAGCCAAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGGAGGAGTGCAG ATGGTA
WI-21079c	166 G A ---	---	AATGAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTGCTCACTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/G/A/AAATTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGCAAT

[illegible]

WI-19891c	172 C G	TGTTGGTGTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCGTTGGTGCCCTCCCCCCCCG ACTCCTCTGTCTGGGAAACGTGGCTTGNCTCCAGACACGTGTGATGCCAGCTCTCCTCAGCGG AGCTCCGATCCCTCAATTTGCCATCTGTCTGACTC/GJCGTCTCCCGGGCGTGGGCGTCTTGT CAGCGAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T	GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGGG/C/JGCAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCAACCATACTATGGAGAAATACAGCTAATGAAGTGGTGGCAGAGCTTTGGCCGTGTGA GTGCCCGAGGGTAAAGTCTCTCTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G	AGCCATACAATGGATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACCGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53 G A	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/C/JTCAAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACGAGGATTTATACCGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTTGTTCCTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130 T C	CCACTTCAATATTTACAAATGCTCAGCGCAAAATATGAAAAGCTTCAACACTTCCCTTTGTA ACTTGTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAAGTTGAA/T/C/ TACTAAATTTTATGATGTTACTCATATTTTATTCATATACATTTTATGACATCATTTGCCAATACATA CATTATTTCTNTAATTTATTTTACAATAAGCCAACTCTGTCATGCAG
WI-20768b	190 C T	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGAGGGCTAACAGGACCTCCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTTCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGACCCAGAGNTCAGCACATCTGCTGGGA/C/T/CAGGGACTC GTAATTCGCCTTGGTCCAACTCTTCTATGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T	TTCCACTCAAACTCCACCCCACTTCTCTGGAAGGAGGGCTAACAGGACCTCCTGCTGCTGCTGC TCA/C/T/GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGACCCAGAGNTCAGCACATCTGCTGGGACCCAGGACTC GTAATTCGCCTTGGTCCAACTCTTCTATGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T	TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCAATTTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTTGTTGTCATCTTTAAAGAAA TGTCTTAACATACCAAAG/ATJAGTGGAAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTCCTGACAGT GGCACAATCCCATCCATCTTCAGGCCTTTTAATAAGGTCAATTATGAATCTGAATTTCTTGA/GJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTGCTGCGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAGGATGAAATTTCCACATTTATTTNCTTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTCTATG AA/CTJGAGCGAGGAATGGGCATGGCGCTGCGGTACGACCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGTGTG/CJTTCATTTGCAAAATAAACCCCA GACCGGGTCATCTTTCAGTTCCTTCCAGCTCTATTATTTATGATTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-2290a	136 C T ---	---	---	GACGTACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGSSCCTCTAAGCACCG GCCAGTAGTGGGAATGCCATGCATGGGTAGTGGGATCTGGGGGGGTGACGACCTTGCTTTT [C/JT]TCCAACTCTCTCTTTCAGCAGAACTTTCGAGAGCCCCCTTNNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCCAAATGTGCTAAGTCCCAATTCAGAGCCCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA/A/GJGTTTGAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGCTGGCACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCACACCAAAAAATGGCAGCTGGGGCTAAGGCATATTAAACAAAGCTCCAAAGGACCCCTT TCACTTGGGCTAGCATCCAGCCTCTCTCAGCAAGGCGAGGATTGGGT[C/J]CCTTTGTGTTTTCTG AACAGGGCCCCAGGGCAGCCAGGCATGCOATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAGGGGCAACTCTTTAAT/A/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCCTTACCAGCTACACTTTACCTTGATCTATATAAAGTGTAAATTTAGAGT AAATACATTTGGCTGTAAAGTG[C/J]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGCTTATGTGTTGAGACAATCAAGNCTGCCCTTCCAGGCACAGCCCCAGTGCT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCCTTTCTGTGTTTCGTATTTTCCCTTTTGTGAGTAAATNAGCAATACACTGAT/CJTGGA ATCTGCATGATTAATAACATTAAACAGTTCAATAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAAATATCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGCACATTCTCCTCCTAGTT T

WI-21763b	154 A G ---				CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT/G/CAGACATTGCCTGTCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---				CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---				CAGTCCATTTAGTCCCCAGTCGAGGGTGCATTTCTCTTATCTTGTAAAGCCACTTGGGTAA[AC] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGTCCAGTCCCTGGAGGGAGGCTTCTTGG AAAT
WI-22449	74 T C ---				CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/C/GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---				CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCTGGCTTCTGCTCCAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGC/A/GJCCCCACAGGCTTCTCTGTT TCCCAGTCTGATGGATTACGCAAGACCTTACACATTACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGTGCTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---				CACCTGGCAGTTGATCAGATTGTAGGAAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTTCTTCTTAAG/C/GJGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---				AGCTTTACAACAAAGCGAGGTTTAAAGAGGCTGAGAAGAAATTCACAACTATTGACTATACAGAG TCTTCAATCCAAAAACAGTTAATAGTAACCTTGGTGGCACATACAAATGCATTGAATACTCTGTAT TATTCAGTAACATAAT/C/JAGGNTCCTGCATCATTCTCTTCAACA
WI-22250b	132 C T ---				ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTGTAGTGGTTATTATGGGTTCTCTGCCTCCTGGCTGTGTTATG[C/T] GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---				ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCACTG/JATAGTGGTTATTATGGGTTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---				GCAGCCATCCTCTCTCCAACACCTCCAGGCCAACCTGGGGCCAGACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGAGTTCTGGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTTGTGGACTCCAGCCAGGGGATGAGGCCAGCCCGAGAACCTG[C/C]AGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGT

UTR- 04932-2a	149 C T ...			GCAGCCATCCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCCGCTGGCCCGAGTTCTGGCTCTCAGGACGTCGCCAGCAAGTGGA GCCAGAGGTTTGCTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTCTGGGAGGTGAGGAAGGAGT
stFIBBb	412 G C ...			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGGTGTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341 T C ...			GTGAGGAAGATGGACCTGGACAGAGATCAGCTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACCGCCCTTGGCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACAGTCTGGTTACGATGGTGTGAGCTTCTTAGAACCTTCCATGGTT
stIGLV2	61 T C ...			GTCAAGAGGACGCGCTCTGGGAGCTCTCCACCATGGCTGGGCTGCTGCTCTCAGTC/CJCTC CTCACTCAGGACACAGGTGAGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTCTC TCTGCTCTCAGGCTCAACGGGGCCAGCAGCTCACTGGCATGT
stSG1001 7c	70 T C ...			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCCACCATGGCTGGGCTGCTGCTCTCAGTC/CJCTC TA/T/CJAGGCATGAGCCCAACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTCTTAATOC
stSG1001 7a	33 G A ...			GTTCAGGCTCATCTTGAACCTCTGGTGTCAAGCGATCCACCATGGCTGGGCTGCTGCTCTCAGTC/CJCTC GATTATAGGCATGAGCCCAACCTGGACACAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTCTTAATOC
stSG1002 3	63 A T ...			TAATGATAATTAGGGCATCTTCCACACGAAGATGACACAATTGACCCAATATCATTTGAGGC/A/T AACAGTTTGGGCTGTTTTCCAGTAGTAGACAGTGA
stSG1009 6	36 G C ...			GTGGAGAAGATCGTCTTCTCCTCCATGACCG/CJGGCTTCCGGGCCACCTGTGGGTTTTTC ACCCGAGACGGCCTTTGTAGGACCCACTGCCACTCGCTGTGGCTGGGTTCCGCTCTCTAG GGCTCGAGTGTAAAG
stSG1011 8	107 C A ...			TAGGCTTAACCTGGAAATCTACAAGCCAAAAGTCCCTCCCTGCTGAGGGCAGTACCCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATCTCTGGC/C/AJCTCAGCCCTCAGTCTCTCATTTCC ACCAAGCCGCTGGCTTGTGAGTTTTCTCCCAAGTGA
stSG1012 0	89 T C ...			TAGTAGGTAAGAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACTTAAATAT/CJGTTGTGTAATCTGATTTTATCTCGTCTTACAAATG
stSG1017 8	42 C T ...			TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAAGTCCG/CJTGAGGAGGAGAAGTGAACAGGAA TCGATTCTTTGCTTTTAACTGCCCTTAGTAGGAGATGTTAAATACCTTGGC

stSG1019 3	136 GA ---	---	GGACAATACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGTATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAAACCTTTTAC TIG/ATTTGAAAACTGAGATTAAAGTTGCAAAC
stSG1020 2c	143 GT ---	---	AAGCTAACTTAGGTGAATGGTGCCTCAAGGTCTTCCGAGGGAAGCTCAGTCCCTGGCTTGGGAGAGTCAGCCTTGGTACCTATAACGGGCTCCAAGCTAAGGGCTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA/GTTCAAGACCACAAAGGCAGATGCCACTGCTGCTCTTCTTCTGCTACTTTCT
stSG1020 9b	75 AG ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATTCAAAATAAACTAAATCTCTCTTAAGATCCCACCTTATTTTTA/GJCTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	TCTTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAAATCTCTCTTAAGATCCCACCTTTATTTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACA/T/CJGTGAATATTTAAAGAAAGTTATATTTGTTTGACATAATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 AC ---	---	ATAGGTTTCAGGAACAAAATCAATTAATGGAAAAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACCTTAAGAGTTTCTTTCTCTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAGGCACCTATTAAATGAGGGAGGAAAAATCTACCTGTACACAAAAATCTGTAGTTAACAGCATCTTCAATAAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG/A/CJATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	TTTTTGTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACAACAGTGAACAAAAATATGGCCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACAGCAGGCAATTAGTCAATTAAAAAATAGTACATGTTA/T/AGTGAATAAAAAATTAATTTACAAAGGCTTT TCCACTCGTGGAATTTGATTCCTTTTGGAGGGAGTAATCCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAAACTAAGGCCATTCTGTGA/GCJTATTTTAAAACTTGGTGTTCACACATAATGATCTTAAAAAAAATGAATTACCAAAACCAAGATTCTCTCTAAATGAAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	TGCAAAATGTGAGAAGGCAGGAGGGGCCAACCCCTGGACCTCATCTCTGTCTAGAATGTGAGGTGTCAGGGATGCTTAAGTCTCTCTGCGAGAGACCCGAGGTGCAGAGATGATTCTTCTCA/CJCCCTTCCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTGAAGGCACCTGCCCCCGCCAGACCCCTTCTAACCTCTGCACACTGGAAGGT/G/AJAAACCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T	GTAAACCTTGCAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAA[C/T]TGACATGGGGCCAAAAGACTTCCAGACAAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST38458 6	65 A G	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAAACCTCAGGCTGCTCCTACTCA[A/ G]TGTGGTTTCTAGCCTCACTCGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAACTCACTCTCCA
EST36745 3	56 A G	GAGGGGAACTTCAAAGAGGATTCCAAACAGTGAAGCAGAATCATGGGGCAAAGT[C/A/G]CTATGG GGCCAGACTGAGGTTGGAACACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGGAGTAGCCAT
STS- R37410c	201 A T	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGTATG T[A/T]TTTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410b	139 G T	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 C T	TGTGACCATACCAACCTATGCAATAAAAGAAAAAATCCTCA[C/T]TTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAAATTTATGGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R42778	74 C T	TATCGTGGGAAGTTCCAACTCATCTTATGCTGCTTTTCTACTTGCTAATATTGGATGCTTCTTGCCA GGCTC[C/T]TTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C/G]TGACGA AGGTAGCAGCACACTGTGAGTGCACCTAA
stSG1026 6	55 T C	GAAATAAACTAAACCTGCAAGCAAAATCACTGTTAATAAGAAATTGTTCTTCTGTTT[C/G]GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGAGCCCAATGAGGTCTCAGAAATGCGGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70 T G	GTATAATCAGCATAGCCAAAGCCCTTTTAAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT[G/A]AGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A	CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTACGCCAGTTGGAACCAACATAG TTTCATACCACCGTTGAAACCATGTGTTTATATGCAATAACAGCAAAATAATTTTTCACCT[C/A]TTG TCAATGCCAATGCATTGAAAGGCCCAAGAAAATGAGAAAAGGATAACAAACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCACTCCAT/CJGCAATTCCTCTTTGG CTACTATGTCTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAGGAAGAAAGGATGCATTTCGG GCTCCAACTGTCTAGGAAGGCTAGACCTCAACACCA/CJGCACTCCATTCCTCTTTGG CTACTATGTCTTTCCCTGACTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---	---	ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAATGTTTTATAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCACTTCGGGAGGCCAAGAGA AGGATCGCTTGAGCCAGGAGTTGACACAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTC[G/A]AAAGTATTTACAGACCAAAAGGAGGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCAATAATTTGAACCTAGTTTGTCTTACGCGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGCCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TAAATGTCATCCAGGGAGGGGCCAGGATGGAGGGGAGGTTGAGGAGCGAGAGGCAGTTATTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTT[G/J]CAATCATTAAGAA GACAAAGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTGTCG
stSG139	69 T C ---	---	TCGTCTCTTTCCAGTGTCTTCCAGAGCATCCCATGATGTTGTGACCGACAGCACTTTGTGTCT T/CJGCTTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCCACTGATTGTGTACTGTCTTGCTGCCC GATCTGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTTGTCAATCCCT TGGCTCCTCCACTTCAGTTGGCTTCTGTCCTCA/T/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGTGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTAGGTCCJAGJCTCCCTTGCATGA AATGTGGGAGAGGAAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTCCACGATATATTACTATTAGTCTAAGT/CJTTTAAATCAAGGTTGAGA ATGACGAATCAAGAAATTTCTTACATACATAAATGCTTCTTCTAGTTCTGCAGATGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA [C/G]AATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCCTGA
stSG1696	67 C G ---	---	

stSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTTACATCAGTTGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCACAAATTAATACTTGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCCTTTACTTACATCAGTTCCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCACAAATTAATACTTGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 AG ---	---	CTTAATGCCCTTCTCTCTCTTGCACAGGAGACACAGATGGGTACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTT[A/G]GCCACCACCTTCTCTCCCGGTCTCCCAAGATGACT
stSG2022 a	86 TC ---	---	TGCTTGAGGTTTCAAACTCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATACAT[C/A]ATTCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTGT TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGGACAGTGGGCTCAGTTGGGGGTTGAC T
stSG2076	104 CG ---	---	AAACGTTGTCCCAAAATGTGTTCAAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAGTTTACAA ATTAGTTATAAACACATTAAAGATATATTTGACATT[C/G]ACATCACAGTGGGGCATTTT
stSG2108 c	71 AG ---	---	TTGAGCAACAATGATTGCGAATTTGGCAGCTCCAAACCAAAAAATGATT[C/G]GAGGGGCTCCACAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 TC ---	---	TTGAGCAACAATGATTGCGAATTTGGCAGCTCCAAACCAAAAAATGATT[C/G]GAGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 AG ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTA TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGATGGCGATGGTGCGAGTGGGT GCAGTTCCCTGTGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATATTATTTAAGGC AGTTTCAGAGCAGCTGGCATTTGTTGCTCTG
stSG2141 a	113 CT ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGTGTA TGAATCTGACTGTGTGAAATAATCTCAGAATGGCAGCACCCTGCGATGGCGATGGTGCGAGTGGGT GGTGAGTTCCCTGTGTCTCTATTGCTTGAAGAGAGAAAGTTCCCTATTATATTATTTAAGGC AGTTTCAGAGCAGCTGGCATTTGTTGCTCTG

siSG2148	50 A G ---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTGTAGACCGTGATTTC/GAAGAAACAATAA ATGTGGATTAGAAAGGAACAACATCCATTACTGTATTTTCGATACCTTGTGATGTTCCACAGACGAGCTC ATCAC
siSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT IC/TGCCCGCTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGAGTGGAAGACCA
siSG2189	41 C T ---	---	CAAGTGTGAAGCTGGGATTGAGCCTGATATTCACACTA/C/TCTACATCCCTCCAGTATAATA GGAACCTCATCGTAACTTTGAGCACCTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
siSG2200	49 T C ---	---	TGTTGATGACCATAGAGGATGCAAAAGCTCCGGGCTGGTTCTGTATGATG/CJT/TATATTTATGTAT AATGCTTACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
siSG2243	85 G T ---	---	CATTTCTGCCTCCTGCTTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAAG/GTTAGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
siSG2257	65 A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGTCTAACTCTGTGAGGCGGCTATCAGAAAGGCGAG/A C/TGTGAGGAACTCTGCCAAGCACTGGGCTGCTGCTCAGGCAGAAATTCCTCCT
siSG2306	67 A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATATTTTACA [A/G]TATGCTCCATTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCAGTGTTCACAG TTCTCCAGAGA
siSG2334	70 T G ---	---	GAAAACTACCCACAGCATCATGTTAAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAAAT/GTGCAGTGGAGGGGCTGTGGAGGGGTGAATG
siSG2339	63 T C ---	---	AGAGCAGATGGTGAATCAACAAGACCTCAAAATGCTTGACTGCGAGAAGTAAGTGTGAC[T/C] GTTCTCAGAGTCAACATTACGGTGACTGTGCTATTCTGGCTGCTCCTATTTCATCA
siSG2465	76 C T ---	---	CAAGACTAAGAAGCGCCAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA/C/TTACAGATTAAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGGTATGCA
siSG2549	140 T C ---	---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATATT/CTACACACCCACCCCTTTTAACT
siSG2577	123 T G ---	---	AATTGCCAAATGGAAAATCCAGAGGATTTTAGACCAACTTGGCCCTGTTGCAATCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA/T/G]GAACAATC CCGGCCAGATTAATTATT
b			

stSG2577 a	121 C T	AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATCCAGTTTGGT CCCAATATAGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58 G A	ATCTCCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTCGGGAAATAAACCACTGTCCAGAGAGAGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101 T G	AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTATTAATAATTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCAATAATCA[T/G]TTTTTTTAAATCCTGGGTGTTGAAAGAAC
stSG2776 a	65 G A	GTGGCCGATCTTTACTTTTCCAGAAAAGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCCAGGAACCTCAACAAGGACACTGCTGGCCAACCAAAAA ATATCCACTAATCCCGAATATAGTAAACCCTGTCTGTCCGAATG
stSG2791 b	109 G T	AAGGAAAGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATACCTCTGAACGGTAAACTAGCAATTTTAATAAATATTTGTTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G	AAGGAAAGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTTC TATTATACCTCTGAACGGTAAACTAGCAATTTTAATAAATATTTGTTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T	CCGCAATTTCAACACACATTTCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACA[C/T]GAAACAAAAATAAGAAAGAAAAACCCATGAAATGCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A	ATGGTGCATTGTAAAGGCAATTAATACTTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCTCCCAT
stSG3031	71 T C	ATACTCAGGGGGCTGAAGGGCAATGTGAAGAGTGAAGTCAAGTCTGGCAATTTCTGTGGTGCAGC AAAT[C/G]CCCCCTTTATTTAAATGATTCCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A	GTCCCAACTCCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAAAGCAGGCAAAAGGCAAAACTGGCTGAGGC
stSG3092	94 T G	CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCACTATTGAAAAACAAGCCCAAGTTC CAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTTCTTATGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGCGAGATACGAGCACCTG CATCTTTTAGTCAATTTGTAGTGGAGT[C/A]GTTGGGGTGTAAAGTGTCTGAAGTGAAGTAG
stSG3245	160 G C	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTGTAGAGGCCAGTGGGGGTGCCACTTGGTGTCTACCAACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTTCATGCTTTAT

siSG3265	42 T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTATTTATAAGGAAATCAGCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAAGTACAAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
siSG3269 b	141 C T ---	---	TGTACTTACTGTGTCATCCTATCCATTCCCTCCCTGAGCTGGAGTGTCTTCCAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/TTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
siSG3269 a	24 A G ---	---	TGTACTTACTGTGTCATCCTATCC[A/GTTCCCTCCCTGAGCTGGAGTGTCTTCCAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAACT
siSG3284	130 C T ---	---	TTAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATATTAAATGACTAAATTACAAAAAGC ATAAAATGTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCC[A/C/TT] TCCCTAACTTTTGTAAATGCTGTAATGGGACATTTGTGTTTGTATCACC
siSG3292	99 A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATGGACAAGTGAATTAATATCTAA[A/TTTACAAATCAATAGCATTTTCCTAACCTCAA TAAATGTCATATCTTTAGTCTCACT[C/A]CCAGTGTATCCATTTCCCAGCCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGACATCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCACTGCTTCATTCCTTTAA GATCCCAGTATTATTTCTAAATTTGAACCTTGTGTTGTGGAATAAAAAATCTGAGGACCACCTCAGAG GG[C/TTATAAGGGAACCTCTTTTGTCTTAGTTCATAAGGACTTTCT
siSG3369	69 C T ---	---	CAAGACTGTAAAGACGTAGGCTTGTGAGAGTGAAGGAGGATGCTCGAACTTGGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC[G/TTCTGGGT CAAAGTCTAAGAGGACAAATAAATAGAGACT
siSG3398	125 G T ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43 A G ---	---	GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTTCAAGCGACCGTACCA CCTGGCCTCCCAAGTTGCTGATATTACAGGTGAGCCACTGCCCCCGGAGCTTTTAACTGAAT GTTGAAATCATTTCTGCTCTTTGCTGGGTAACTGAT[A/CAAGTTGCTTAACCTTTGTGAACCCAC TTTCTCTATCTGTAAACAAATGGACAACAGAACTTTTCTCTTCTCTC
siSG3424	173 T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGATGGAGGCTTCACAGA ATGAGTGGCAGAGAGGGCCCC[TTA]GAAATAGCTTACTCTGTTTTCCTATC
siSG3436	88 T A ---	---	

stSG3463	103 C T	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAACAAATAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAACTTGCCTTGACTATATTA CTGA
stSG3491 b	71 G A	CAAGATACTTCATTGCTCTAAGTAGTGCAGTGTGGCAAATATTTCTACGAACAAGGACGATTTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTTAATCTTTTACTGGCACCTGTGGATTTCTATTAACTCATTTATACTATTTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T	TAGCCATCTTACTCTAGTCTTTTGGGTTTTC[C/T]GCATATATGTGTACAAACACACACACACC CCTAATTCCTCAAATGCTCTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213 A G	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCCAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGAAACGCATCTCACTGTCATTTCTATTGTTTAAATGAGCTTG TGCACCATTAG[A/G]TCTCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112 G A	GAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C	CCTAGTACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G/C]ACCG CCTGTAGTCCCTACTTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101 T C	ATATAGTGTGGTAGCATTATAAAGTCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCACTGGCACAACCAACCCCAATGA[T/C]CTATTTCCAAGATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590 a	70 A T	GAGAGATGAGCTATTTATCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCTGTAGGAACACATTCAGTTTCTACACT
stSG3619	78 A C	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTGAATTCATACGCT TCTGTCAATT[A/C]AACAACTTCCAGAGAAAACTGGGCTCTATATTTAAG
stSG3644	40 T C	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT[C/G]GATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAATAATAAGTTATCTGGGGAACCGCCATTTGTCCAACATTTACTAA GTGCCTACTA
stSG3646 c	70 G A	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGATATATGATGATAACAATAATATGTCTTACT GGT[G/A]TATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTTTTGTA

siSG3646 b	55	A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA/GJATATGCTTT ACTGGTGATATTAACCTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3646 a	43	A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/AJTGGATAACAATAATATGCTTT ACTGGTGATATTAACCTTTGATACCTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
siSG3693 b	85	A C ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCCTACGAGGCA/CJTGGCCCTCCGAGACTGACGATTATTAACCCACCCACACGGAAGG
siSG3693 a	30	C T ---	---	ATTGTTTCCCTGAACATTCOCGTGGTCTCC/CJTCTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAAATATCCTACGAGGCA/TGCCCTCCGAGACTGACGATTATTAACCCACCCACACGGAAGG
siSG3698 b	145	G A ---	---	TCTGGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTGTCTCTGACTTCCACCAT TCACTGACTTTTATGGCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
siSG3698 a	51	C G ---	---	TCTGGCCCTTTGTGTTACCCCTAGAGAGATGGCACCCCAATCCCCAGGGTGT[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATGGCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA
siSG3724	107	C T ---	---	ACCAGCCTCATGTGCAGAGGTCTCCTGCTGGATCCCCAATCGAGGCCATCCCTGGGCCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
siSG3725	104	G A ---	---	GCCAAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTTAATAGCACAGTCAACAGCATTTAA ATCAATATATATTACCAGCCCAACAGCAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
siSG3751	128	G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
siSG3787	49	T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA CACTGAGGGCATAAACCCAAACAAAATAAAATAAGGAGTATAGGCTAAAGCAGTATCTTCCCCT
siSG3880 b	115	G C ---	---	GACAAGAGGAAGAGATGCCACAGAGAGAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGCGC CACCACAGTCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTA[G/C]GGCAGGAGGATGCAG GGCTGGAGGGGAOCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT

stSG3880 a	36 G C ---	---	GACAGAGGGAAGAGATGCGCCAGAGACAGGGCTG[C]GCGAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCTCTGGGAGCAGGCTAGGGCAGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT
stSG3885	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]G]TTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACAGGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAAGTCTTTCTTTCT[C]T[C]CAGCTCAATAGCTTAACATCTAATTC ATGTTTCTCCCTTTCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTCACCAAGCAATTTGTCC[G]A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACCTTCCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAGTGTGA/G]AAATATATTTAAGATTTCTTTGGGGAGAAATCTGTGC CCAAACCTGGTATGATCCCTTACTATTAGATAAGGAACAAATAAACCCCTTGTGTATGTATCA CCCCAA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[G]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTTCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGGACAATGGCAGTGGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGATCCATT TGAACCTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT[C]TGTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCAGTGTACAGCCACGCCCTG[G]A]GGAGGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAACAA[C]G]GGTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCCTAACAGAGATTATTAACCTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGAGTACTATTGTCTGCTAGATGTATTAG[G]TATAAAAA GTTTGCTTCTGTAACTATTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGT[C]G]GATACTATTGTCTGCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAACTATTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G] A]CTTTTCCCTCAGAGAGGCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	...	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT/GATATATTTT TACTTCTTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGG
stSG4209 b	128 G A ---	...	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAAGC AGGGCGGCCACTCCAGCAACGAAGCACCCCGAACCTTGACAGGCGCGACTCCCTC[G/A]GC AGGGGACACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	...	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAAACATCCACATGGCACAA[G /A]CAGGGCCGCCACTCCAGCAACGAAGCACCCCGAACCTTGACAGGCGCGACTCCCTCGGC AGGGGACACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	...	CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGACTCCGCGATGGCTGGGGG GCTATGGCTTGACAAGAGGATGAGCGAGGCGCGGGGCTGCTCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTGATG
stSG4301	81 T G ---	...	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAAT[G/A]GCTTCTGAGTAGTGTCCAGTTCACCCAAACATTTTG
stSG4331 b	71 T G ---	...	CTCACAAGGCCAACACAGAAAAGATACAAATACATTCACAGCTAATATTTAGTTTTATGACAC AGAGT[G/J]TTTCAACAAGTTTAAAGTGCACCTGAAGAGCATGTTAAAAGTTTAAAGTTATCATT GGAGAGCAGATTTCTGGCCTCGCCCTTGATCTGTTGAGGGGTGTC
stSG4340	76 G A ---	...	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAAATGATACAGAAAGTCAAAAACC ACATGTTCT[G/A]TAAAGTGGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	...	TTCCCAACCATTTGAGTGACAGAGCTCAGTCAATGCAAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGAAATTTCCATAAGGGATAACTGCATCTTTTGC[A/C]CCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4361 a	24 T C ---	...	TTCCCAACCATTTGAGTGACAGAGCT[C/J]CAGTCAATGCAAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAGTTCTTGAAATTTCCATAAGGGATAACTGCATCTTTTGCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAAAATGTCGAGG
stSG4376	73 A G ---	...	TTCACTGCTACTGGTTTCGGTGTCTGAGTCTCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAG AACAGI/GI/GTGAAGTGGCTCTGCAAGAAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	...	GAAAGCCACAACACTCCATAGCCAGAGAATGACAACATACGATTTCTTTT[C/J]TCAGTCTTGTAGT ATCCACAGTAGTGTGTCTGTCCATGTACAAGTGTCTGTCCAGAACCCCATTAATTCATGCC ACCAATGGTTCTGTATGTGATCCGATATTTTTCGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG[G/J]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGGTGGCTTGT CAGCTGGGT
stSG4410	79 A G ---	...	

s1SG443	65 C T ---	---	AGCAGATCAGTCAGCCCACTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
s1SG4430 a	54 A G ---	---	TJGTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGAGGGAATAGGCAC AAATGGAACTTCTATCTGGCTGTCTCTCAGGTC
s1SG4448	99 G A ---	---	ATGCACATTAAATGAATGGCCTAACTACTGGAACTTTAGTAGTTCTATAAGGTJ/GJATTAACATA GGTAGGATCCAGTCTCTATGACAGGCTGCTGAAGAACAGATATGAGGCATCAAGAGGGCCATTTT CCTCCCTCCCTTCTCTCCCTTCCAGTCTTTCCATACTGTCCCTCCCGCCCAACCCAGGCTCT CGCTAGCCCTGCTGGGTCACTGCG/GJATGGGTAGGCCCCCAAAAA
s1SG4449	92 T C ---	---	ATTAGCCATTTCATCTTGCACAAATGCTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT TAACITTTGGACAACTAAACCTTAT/JCTAGTGACATTGCTGTCTAATAATCAAATACTTCATCATA GGCTGAACATAATTATTAAGAGCAAGTTACCCCTCCC
s1SG4467	42 C A ---	---	CAGACATGAGGATGGCCCTGTCTCTCTGGGACAGAGCCCA/CJAGATGATGTCCATGTTTTGTGT GAATGAACTCAACACTCTTCAGTTTTAGAGTCATTTTCTGGTATCGAGCGACCACACCGAGGAG CACACCTGCTTCCAAAGGCTGCTGCCCTCTGACACAGT
s1SG4475	21 A C ---	---	ACATGTCATTTCCTGACCAGG/JCJTATTAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGGA TTAAGAGACACAACTGGACTTTTGTCTTTTACTGTAGCACCCAGGTTTCATG
s1SG4477	32 A G ---	---	GTAACATTCTGGGGTGGGGTGAGACAAACA/JGJATGAACCAATAATTAATACAATTATACATT TCAAGGAGACTTTAATCTAGGTTAATGTGAACCGCAGCCATCAATGTTGTGAGGAAAAAGGGAGA TGAAGTCTGCTCTGGGCAACGTTGGCCTCATTCAGTCAGACTTGGC
s1SG4531	79 C T ---	---	TGAATCAGAGCTGGGTGGGAGCTCAGCGAGGGAGGCTGGGGCCAGATGAGCCGCGCGGGGA CAGCAGCGCTG/CJTGCCACGTCTGGCGTTGGTGAAGAGGACATAGGCTGCCCTTGGACTCGATCT GATTCATTGACAGGGGAGACGCTGTGTCAACAA
s1SG4550 b	86 G A ---	---	TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCACC/JAICAAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
s1SG4550 a	85 C G ---	---	TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT AAAAGAGACAGTGGGCAC/CJGCAATTGGAGGGGAAGCGGGGCGAGGTTTTAGAGAAC
s1SG4590	47 A G ---	---	AATCAGGCACAAGCTCGGGAGAGAAAGCCAAAGCTCTTCTGCAC/JGJATGGGAGGGAGACAC CATTGAAAAGGCATCGTTCTCTTCATGCAAGCGAGGCTGGCTCCACAGGCAATGGTCTCCTTG AATCTGTATCACCAGCGCTGGT/CJCAATGTACTAGTACTTCCACAGGATTTTTTATACTATTC CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTACATTTATCT TAATATTCTGTTCAAGATGCTCTGAG
s1SG4623	22 T C ---	---	TAAAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTGTGTTTTTATGTTTTTACAGATTTAAAG GTATTTCTTTCTTAGCTTCTAAATTTTGTAGTCAT/JCJATCAGAAAGTCTCCCTACTCCCAAGGTGA GAAAGGA
s1SG4843	102 A C ---	---	

stSG4850	38 C T	...	GGAACTCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC/CTGTGCACCTTGCAGGCCACGTCAGGAG AGCCAGCGTGCTGTGGGGAGGTTTCCAAGGTCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G	...	AACCTCTGAAGGGGGTGACCTCAACCAGCCCTTGTTCTGTGAGGTCTGCTTTTGCAGAATGGCCTG CCCTGGGACTGGAGCAG/AG/CTTGGGTGAGCTCTAGGTGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A	...	ACTGGACTGGCTCGCTTGCTGAGCCGGCTGAGCGCGTGGGACTCGGGCTGACCACCTCGCTCTTCAG AGACTGCGCGCGGTGACCACGACTACGCTCTGCC/GA/GTGGGAAAGCAGAAGCAGGACC
stSG4896	112 C T	...	AAACAAATCAAAACCCAAATCCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCTCT/CAGCCACAGGCCCTCGAGG AATTAATGACTG
stSG4932	22 G A	...	ACAGTCCGATGGTTACACAAAT/AG/TTGTAATGTATTAATCCCACCTACGAATGATTAAAATGA TAAATCTTATGTTTATTTATCATCACTACCAAAAGGCTGTGGTGCAGGGGTGCTGTTTCTGTCTCT
stSG4950	24 A G	...	TCATGACTCCAGGAAAAGTCC/TA/GTCTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTCAAGG
stSG4957	136 G A	...	AGATACGGGCAAAACACTGGGATGGCTTCTTGACAACTTAAGAGGTCTCCGAGTTATATTCTGGTT GGGAAACACTGACCCAGCCCTTATTCTTCAAGGACTCTAGTCACTTGGCAAGGAGGATTCATGAGCC CC/G/AGTGACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T	...	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAGTA/C/TTAGAGAGGGCATTGAGCCCAAGTCAGCAACACAGACAA
stSG4967	72 A G	...	ACTGTGCTCTCAGCAGATTACGGGTGTCAGGGCTGTTACCAAACTCAGTAGGAGTGCAG GGCT/AG/TTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTGTGTGC AACCTTG
stSG4997	22 T C	...	CAAAGGAGAGTAGGAGCCCAAT/C/TTTAAATGGTTTCTCTCCCTCATGCTATTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T	...	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAAACA/C/TTATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345	107 G A	...	GCTCTGTCGAAGAAATCTCCAGGACAGAAGCAACAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC/CA/ATAGTTTCAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACAATTTGCTCTTTGGCCTGGTGTGGACAGAAAAGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG8362	88 G C	---	---	---	TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAAGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTAG/GJAGAAAGGGAAGGAGGAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T	---	---	---	CACATCTGTGTTTCTGGAGCAAAAGGGAACCACAGAAAGGCCAGGAGTTTGGGTGTGCACTGG/GJT GTCTTTCAACTGGGTGGAAACCAAACTGAGTCCTTTGAAGTCTCGCTCTGAGGCTGCAGAAGAATAGA TGCGTT
stSG8022	53 G A	---	---	---	AGCTCCTGACTCCCTGTTCAGTGACGTGCATGTTGGTAGCCTGAAATGGACCAC/GJGTGGGAGTTAT TTACACCATGGAACTGGAAACTCTACAAATCAATCGTTTATTTCTTTATTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67 G C	---	---	---	TGATTGTTAGGATAAGTGGGCAATTGTGTTACAAATTACTTCCAAGAAATTCAGAAAAATTGTGTGT G/CITGGGAGGCAAGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGTGGTAAAA
stSG8064 b	46 C A	---	---	---	AGCTGGCTTCTCTGTGCTGTTTCGGAGGCTTCACGCTCGIC/JCCTGGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAACAATGCCAGGGAGAATCTCTGTACATCAACAGGGAACA
stSG8064 a	23 G C	---	---	---	AGCTGGCTTCTCTGTGCTG/GCJTTCGGGAGGCTTCACGCTCGCCCGTGGTCCCTGGGTGGCC TGCAGGACAGGGGTGGGAACAATGCCAGGGAGAATCTCTGTACATCAACAGGGAACA
stSG8072	59 A G	---	---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTGTCTTAGGG/JGJTGGC AGAGGCAGAAAGGAAGTCCGAGTATTAGTGCCGCATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G	---	---	---	ATACCCACACACCCCCACTCAACCTTGATCAAAATCCA/JGJAGTGTAACTAAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138 T C	---	---	---	AAGGCTCCTTTGAAAGCATGGTTATTGTTCCATTAACTTGTTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCAATATTTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA TGA/TCTGTCAATAATCAATAATGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110 A G	---	---	---	CAGTGGTCTCAAACCTCCAGCTACACGAGGATGGTCTGTGCTTGTTAATACACAGATGACTAGGCC CACCTGCGGAGTCTCTGTTGGAGTCTAGGCCTGAGAAATATTC/JGJTTCATAACAAGTCCCAGGTGA CCCTGAGGCTCTTGACTGGGAACATGCTTTGAG
stSG8130 b	96 T C	---	---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAAGTTTCAAATT GACATTCAGACAAGCGGTGCCTGAGCCT/CJGTGCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G	---	---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGA/JGJGGATGGTGGCTGCTTTTAAAGTTTCA AATTGACATTCAGACAAGCGGTGCCTGAGCCTGTGCTTCAGATCTTCACAGCACAGTTCC
stSG8145	124 T A	---	---	---	TTGTGGACTTCAAAATCTTTCCCTTCAGATTTTAAAAATGCATTTATGCATGTACATATTTTAAAAATTT AGACACATTTAGAGAACACAAATGTGAACACACAAATCTAAGAAATGAATGAGATGTT/JA/CTGAAA TCTGATTCAAACACTTATCTTAACTGACTCTGTCAATCCCTGCTGCTGTAAGG

stSG8145	97	C T	---	---	TTGTGGACTTCAAATCTTCCCTCAGATTTTAAATGACATTATGTCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTGTGAAC[C/T]ACAAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACATTATCTTAAACTGACTTCTGTCAATCCTCTGTCTGTGAAGG
stSG8150	36	A G	---	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAAATAGT[AG]ATAAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAATGTTTGCCTATTAAATACCATGCAGGAAAT GGGAAAT
stSG8340	30	C T	---	---	AGAGGATTATGGAGAGAGCTGGCAGGATC[C/T]CAACATTATGACCCCTGAACCTCCAGAACCTGGAT TCACTAGAAGGAGAGAGAGAAAACGCTCATCAAAA
stSG8466	111	G A	---	---	TGTGTATTGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTTGCACTACCT[G/A]TGAAGCAGCACAGCATTAT TTGAAAG
ESTD-ACE	---	---	GATCAAGCAGTGCACACGGGTACGATGGACCAAGCTCTCCACAGTGCACATGAGATGGCCATATA CAGTACTACCTGCAGTACAGGATCTGCCGTCTCCCTCGTGGGGGCCAACCCGGCTTCCATGA GGCCATTGGGGACGTGCTGGCGCTCTGGTCTCCACTCTGCAACATCTGCACAAAATCGGCCCTGC
ESTD-ADA	---	---	AOCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGTCACCTGTTCTCTCTGTTCTCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTGGCACTGAGCTGCAGACCC GCAGACCAACTCTGAGCTTTCTGGCCCTCTGAGTCTTGTCTC
ESTD-AK-168	---	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	---	---	AATCCAGCACTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTGAGGATTTGAGACCAGTCTGA CCAAATGTTGAAACCCCATCTCTACTATAAAATACAAAATAGCCAGGCATGGTGTGTCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGATCGCTTGAACCTGGAGGCGAAGGTTGTGTGAGCCGAGAT GGCAOCATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGTCTC
ESTD-ANT1	---	---	TCTCCTGTCACTTCTACTCCATTAGTTCAAGGTCAGTGAAGAACTGGGCAATTAACCAAGTAATTCA TGGACTGCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	---	---	CCAGGTGTTGTGGCAGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-APB3	---	---	GGAAGAAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGTGGGCTTTGTGGCAAGCCCTTGTCTGA AGCAGAAGGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCOCAACACTCATGAAGCT GGCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC

ESTD- AT3a	..	--	---	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTATCAGGTAGAGGAGATGGACCAGGTGGAGGAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
ESTD- B3AR	..	--	---	---	---	GGCTGCCAGGGTTCCGTGGAGGCGGCTAGCCGGGCCCTCTGGCGTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGT GTTGCTGACTTCGCTGGCGCAGCCGACCTGCTGTGATGGGACTCTGCTGGTGGCCGCGGCCACCTT GGCGC
ESTD- BA511	..	--	---	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCTGCA
ESTD- BCL2	..	--	---	---	---	AGCTGGATTATACTCTCTCTCTGGGGCCGTGGGTGGGAGCTGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAGGATGGCGACGCTGGGAGAACAGGTACGACAAACCGGAG ATAGTATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGCCCCGGGGCGCCCCCGCACCGGGCATCTTCTCTCTCCCA
ESTD-BCR	..	--	---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GACCAAGAGGTGACGCTCTGTGTCCCGGGAAGGAGGAGGAGGACGAGTGAAGCTAACTCTGCTCAAA ATCAACCATCCGGTGGACACTGTGGCTGCCATCTGCTGCGCACA
ESTD- BRCA1a	..	--	---	---	---	AAGAAGAACTAGAAACAGTTAAAGTGTCTAATACTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTCACCTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	..	--	---	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGAAATGAGAACATTCCAAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	..	--	---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAAATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTACCCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	..	--	---	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCTCTCCCTAAATTTGCTCCGGGAAGCACATTCATCAA CCCAGTCAGTTGGGGGACAGCCATGCAGTGAAGCTCTGTAGCCTTCAACCATGCATTCATCTAA GCTCTGCAAAAT

ESTD- C7	--	--	--	--	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- CB22	--	--	--	---	---	---	GGCAAGTTTTATTGATAGAGAGGAATCAAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTGAACCCAAAGCAAGGAGGACCTAG TAACATAATTGTCCTTATTATGGTCTTCCCGCCTTCTCTCACACAC
ESTD- CB23	--	--	--	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCAAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTCCCGCCTTCTCTCACACATACACAGAGCCCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGCTGTTCCACCCGAGGTCGCTGTTTGAAGCATCAGAAGCAGAGATCTCCACACCCAAAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCCGACACCGTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	--	--	--	---	---	---	GTTTCTTTTCAAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCAAGGCATGGAGATCCACGGACACAGGGCGTGGAGGCCAGAGCCACCTG TGACAGTACCTACATGCTCTGTTCTTGTCAACAGAGCTTACCAGCAAGGGTCTGCTGCTGCCACCC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG
ESTD- CB27	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGTTGCTTTCAGGAGTCTGTGGAGTCTGCTCATCACTGACCTATCTCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCTGCT TTCCTCTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- COL2A1c	--	--	--	---	---	---	AGAATGTATATAGTCTCAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTACTTTCAGGGTGTTCAGGTGGAAAGGT GAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAAGTCAACTCAAGCATATACAATACTGCTTTTG GTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD- COL2A1d	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAACACTGGACTTCTTCTACTGACGACAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTGACCAAAACACTATCATGGAACACG ATT
ESTD- CPT2	--	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCTCATGAAAAC TGGGAGGCCGGCATAGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGCGGGTGGATCAC TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAAACAT

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ESTD- D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTCAAAACATTTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	..	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTTGGACCTCACTGTCCTGGGAGAGGAGGAGTGGGAGGAGACA GAATGCTGATTATCTGGTGGAGAACAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAGACC TCCTGATTTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	..	--	---	---	---	TCCCAGCCTATCGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCTTGCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	..	--	---	---	---	TCTGCTTTGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGTCACAGCCCCATCCACAGCCACCACAGCTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCCGCCAAACAGAGAAGATGGGCATGCCAAAG ACCACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	..	--	---	---	---	AAGCAGTGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGAGCATGTGGCGGGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGCTCAGAGATGCCATA GCCAGAGGAGGTGCTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERB2	..	--	---	---	---	TCTTCAGGATCCGCATCTGGGCTGTTGGGCATGCTCCGCTAGGTGTCAGCGGCTCCACAGCTGG GGTAGGGGTGTGGTCAGTGCGGGGGCGGTCAGACCCCCAAGCGGCTGGGAGGACTTCAOCC CGCTCACTCGTTTCTGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	..	--	---	---	---	ACTCACAGTCTTTTAAGTGAAAATGGTCGAGAAAGAGGCCACAGGAAGCCGCTCTGGCGCTGGCA GTCCGTGGGACGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACACAC AGACTATTTTATAGATTTCTTTTGCTTTTGCAACCCAGGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCATTTCAGAAGTTAGTTTG
ESTD-F2	..	--	---	---	---	GATAAGTACACTGAGCCCCAGGAGTTATTGCCTAGTAGCCCCAACTGTCATGCACGCTTAACCTCT GCACCAATGGCTCCAAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCGGCGGTGCTGGGTCCCAACAGAGGAGGCCGCTGGAGGAGACAGAGGATGGGC TGGATGAG
ESTD-F9	..	--	---	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTATAAACAAAAAC

ESTD- G00H	--	--	--	CGCAGACCGTGTCAGTGTGGGTGGAGTGTGGAGGGAAGGAGGAGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTACAGCTGTCTGTCTGCGCGAGTCGA CTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	--	GTGTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGTGTACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGCTGG AGCAGGAAATGCCAGCGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCAGGTCACAG
ESTD- GNAT2	--	--	--	GACCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAACACAGGCATCATTG AAACCAAGTTTCCGTCAAAGACTTGAAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD- GPPK2L	--	--	--	AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTACCCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	CTGGGCTGCGCCGAGCAGCTGCTGGCACCTTGACGGCGGCCAGGCTCACCTCTATAGTGGGTGCG TATTGCTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCTGGGCCACATTTCTGGCCTTG AGGCCCTGCAGGACCCCAAGAGCCCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAGCTATGATAACCTTAATTACACCTGAGCAAGAGTTCCGGCCTCCGGCTTGATTCC AGATGGAGCTTCTCTTATCCCTGATGTATTGGATTGGCTTCCCTGCTG
ESTD-HT2	--	--	--	GGGTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAGATGTGTACAGTTTGTCAGAGAGATAAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAAOGGTATACAGGGACAGCA AAGCGCAGTCTGTAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACGCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGCGCTGAACCCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	AACACACAAGCCCCAGCGAGAAATTGAACCTCGCGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTGTTGTTTCTCCCTTTCATCTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATCCAGGATATTCCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
ESTD- IGFBP1	--	--	--	ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	TTTACTATTCAATGGATACAGAAATTGTGGAGTCACTATATTCCTATGAACAAAAATTAGATT CAGTGTTAAGTAATGTCCTACATTGTGTGAGTGACGGGAGTGTGGATCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTATTATTATTATTATTTT AGATGGAGTCTGCTGTCAACCCAGGCTGGAGTGCAGTGCCACAAATCGGGTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCCTCGCTCAGCCTCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTCCCGGCTAATTTTGTATTTTGTATTTAGTAGACGGAGTTCACCGT
ESTD-IL1B	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCTCAGGAGCTCTGTGCAATTGCAGG
ESTD- KRT10	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAAAATGCAATTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	ACCTCACCCCTCCCTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	GGGTGATTTTGAGGTCAGTTAATATTCAAAATGTAACCGTAGCAAACTGCATTGGTATTAGA AAATAAAAAATTTCCAATATGATGTGCTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACAGGAGGGCTTCCCTACCAACCCAGA
ESTD- LMP2	TACACACTTTCTTACCCATTCACTGAAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	TGTCAGTGTCCCTAGGGGCACCTCAACACTCCAGCTTCTCAGCTGTGCCCTGTCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATTCAATGTCTCTTCTATCTTTAGCAGCTGTGGGTTTTGTGTGTTT TTCTGTTTTTGTCTAGTATCTGACTACTTTTTTAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MOC	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTTCCAAAGGGTTTGGTCTAGTGTCTAAGTGTCTACCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTCTGTTTTCATG
ESTD-NF1	ATTATCCAGATGAATTTACAAAATACTATACCAGATCCACAGACTGATATGGCTGGT

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ESTD-RDS	..	--	..	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGGCTGTGGAGAAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGCAAGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- FYRI	..	--	..	---	---	CTTGACGGGAGGTACGTCTCCGCTCTTTCATGGACATATGGATGAGTGTGACCATTTCCC CTGCTGACAGTATGACAGCGAGACTTGTCTACTATGAGAGGGAGCTGTGCACTCATGCCCGC TCCTCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGGCATGTCACTACCGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	..	--	..	---	---	TGAAACACCTGTGGTCCGGAGCCAGGTGTGTTCTCTCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTACCTCTTGGCCCGGAGAAGAC ATTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	..	--	..	---	---	TTCACTTTGTGGATTGTTCTTTGTCTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTGAAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTGTGTAATAGTTTCATAGTTTGGGCTTAGATTAAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	..	--	..	---	---	AAATGGTCAGGACCTGATCCACAAGAAGTGGTACCATTTCATCAGGGCCATCAGTTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCACTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTCACACTTTTCTCCAGTATGGATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	..	--	..	---	---	TGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	..	--	..	---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAAGT GCCAGAAAGACCCCCCTCAGAAATCGGAGCAGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	..	--	..	---	---	TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTTGCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGATCCAGACAAAGAGGTCAATAATATTGATGTGCGTTAAACAT GGGTGTTGATCCATTTTCATTTGGCCATAGGTCCTATGGGGATGACA

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ESTD- TYRP1	AGTAGTGATGAAGCTAACGAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTTATTACCTTCTTTCT AATACAAGCATATGTTAGAATTAAGTTCTAGGCATACTT
ESTD- VB12	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCACCAAGACTGAGAACCAACOGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	AGGTAGGAAAGCAAGAGATTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGAGTAGCCCGGACTCTTGACGGTGGCATCTGAGAACAGTGAGAAACGCCCTT CATGTGCTTACCCAGGCTGCAA
ESTD- 814544	TTGGGAAGTTAGAGCCTATATAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGA TATCCCAAAGTTGAAATGTCTCAGTTGCTGTGGGTTAGATGACGAGATTATATGATCCGTTAACCC TCT
EST71770 6	AGCACCACTCTCACGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGCTGTTTTACAA CATCTCCTCCATGAAGAGACAGAGAGTTATTTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGGAAAGG AGTGCCCAAGTCCCAAGGTTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	CAAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTAGCGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG CCCACTCTATTGGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCCCGG GTCACCTC
EST13586 3	AGGCAGAAACTGGGCCCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTTACGACCTTCAAGGAGAAAGAGAGCCAGGACAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAAACAGCAGCAGGAGCAGCAGGAGGAGGATGCTGGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976 7	

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EST11458 6	..	--	--	---	---	---	CCACTTTGGTAGTGCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAATCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTCC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	..	--	--	---	---	---	CGGTCTTCCTTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCACACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	..	--	--	---	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTCGCCCTCTCGGGGGCCCGTGG TCCTCCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGAAACGATGTTCCCTCCAGTGTGGTCAACCCGGACACAAAGGAGAGCGGTTACCCCTGG CAATAT
EST38027 2	..	--	--	---	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCTGTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAAACCTGAAAGG CTGTCTTCTACAGGCTCTAATGATGTTGAACCTGTTGCTGAGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGTGTCTAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	..	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAGAAAGTCAAGTGGTTTACTCCTCATGACCAAAATATCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTCCAGATC
EST78807 7	..	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGTCTATCTCCAGGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAOCCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438 7	..	--	--	---	---	---	GCAGCCAGGAGCCGCTGCACATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGGAGTGGG
EST12839 3	..	--	--	---	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTTTTGGT CCTAACATCTATGACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTTGAAGTAAAGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGTTTCACTTACTTGAATATTAATGATGACTAGCTTAG
EST54419 8	..	--	--	---	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGTTATTTGGTTTAGCGTGGTGTGTTGTTCTACTA TAGTCCAAAGTGAA

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EST26021 1	..	--	..	---	---	TAATGTAAGCTCATCCACCACCAAGAGCTGCACCATGTTTTGAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAGAGGAGCAAGAGAACATTCCTCTGCAGCATTCTACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTCTTTGCAACAAGACAAAGCAAGCC
EST51212 0	..	--	..	---	---	ATCCTGAGCTCGCCAAATAAGCTTCTTGGTTCTACTTCTCTCTCCACAAGCCCAATTCACITTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	..	--	..	---	---	GTTCGGAATCTCTCTGAAAGTGCGCGGGTTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGAGTGGGTTTAGGACGCGGTCTCTGCGTCATCTTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGTTTAGGAGCGCGGTCTCTGCGTCATCTTAAGCT CTGAGA
EST53018 6	..	--	..	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGGGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	..	--	..	---	---	CTTCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCAAGCTCATGACAAATTTGAAGCTGACATTAACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAAGTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACCTGAACTCAGGGTAAGAAT
EST34088 2	..	--	..	---	---	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAAGAGACCGGCTCAAGG ATCCCAAGGCCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	..	--	..	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTTCTCTCTCCCTTGGG CTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGACCCAGAAAT CAGAGTGGGCACGTGCGTCTACCGCATCTCCCTTCTCACGGGAATTTTCAGGGTAACT
EST74082	..	--	..	---	---	TCAGGGTGGCTGGACCCAGGCCCCAGCTCTGCAGAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGGCCAGGGGCCCAAGGAGGAGGCACTGGCTTACGCTGCTCAGGCTGCTGCTGCTGCTG CCAGATCACTGTCTCTGCAATGGCTGTGGATGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGG
EST45311 0	..	--	..	---	---	GCCCTCTCTCTCCAAATCTGTCCCTATAGTTTCTCTATTAAAGTGAACATGACATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCAGCTGTGGCCATATTGTAAACA CATTTTCTGCAATCACCTCTTTCAATTAACAGCCCTTATTCAATGGCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
19. The method of claim 18, wherein the determining
25 comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.
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